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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:27:32 ; Search time 1886.59 Seconds
(without alignments)
10273.834 Million cell updates/sec

Title: US-09-917-265-46
Perfect score: 666
Sequence: 1 atgtgcccgccgcgcggcct.....tgagttatctgaattcttcc 666

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	664.4	99.8	669	6	AR151072	AR151072 Sequence
2	664.4	99.8	669	6	E15018	E15018 Canine mRNA
3	654.8	98.3	669	4	CFU49085	U49085 Canis famil
4	645.2	96.9	669	6	AR151062	AR151062 Sequence
5	598.8	89.9	669	4	FCU83185	U83185 Felis catus
6	598.8	89.9	669	4	FCILL12P35	Y07761 F.catus mRN
7	592.4	88.9	669	6	AX076201	AX076201 Sequence
8	592.4	88.9	669	6	AX076483	AX076483 Sequence
9	592.4	88.9	4201	6	AX076477	AX076477 Sequence
10	542	81.4	660	6	AX154614	AX154614 Sequence
11	542	81.4	660	6	AX154621	AX154621 Sequence
12	540.4	81.1	660	6	AX154617	AX154617 Sequence
13	540.4	81.1	660	6	AX154618	AX154618 Sequence
14	539.6	81.0	1426	4	PIGIL12PSU	L35765 Sus scrofa
15	537.2	80.7	660	6	AX154619	AX154619 Sequence
16	534.8	80.3	669	4	ECIL12P35	Y11130 Equus cabal
17	530.8	79.7	660	6	AX154620	AX154620 Sequence
18	529.2	79.5	660	6	AX154615	AX154615 Sequence
19	529.2	79.5	660	6	AX154616	AX154616 Sequence
20	528.4	79.3	666	6	AX154612	AX154612 Sequence
21	522	78.4	666	6	AX154613	AX154613 Sequence
22	518	77.8	660	6	AR008951	AR008951 Sequence
23	518	77.8	660	6	I28592	I28592 Sequence 3
24	518	77.8	762	9	AF101062	AF101062 Homo sapi
25	518	77.8	823	9	AF180562	AF180562 Homo sapi
26	518	77.8	1364	6	AR082685	AR082685 Sequence
27	518	77.8	1364	6	AR122961	AR122961 Sequence
28	518	77.8	1364	6	I28326	I28326 Sequence 3
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32	516.4	77.5	1316	6	AR050785	AR050785 Sequence
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35	514.8	77.3	660	6	AX154634	AX154634 Sequence
36	514.8	77.3	721	6	AR052862	AR052862 Sequence
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38	514.8	77.3	1026	9	HUMCLMF35	M65271 Human cytot
39	514.8	77.3	1645	6	A92078	A92078 Sequence 2
40	506	76.0	690	4	BTU14416	U14416 Bos taurus
41	504.4	75.7	666	4	CEU57751	U57751 Cervus elap
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44	496.4	74.5	666	4	AF173557	AF173557 Ovis arie
45	494	74.2	786	9	CTU19835	U19835 Cercocebus

ALIGNMENTS

RESULT 1
AR151072
LOCUS AR151072 669 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 12 from patent US 6231850.
ACCESSION AR151072
VERSION AR151072.1 GI:15117122
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 669)
AUTHORS Okano,F., Satoh,M. and Yamada,K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 12 15-MAY-2001;
FEATURES Location/Qualifiers

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  Best Local Similarity   99.8%;  Pred. No. 2.1e-189;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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Db          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

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Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 2
E15018
LOCUS       E15018                    669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI .
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
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            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /db_xref="taxon:9616"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

  Query Match             99.8%;  Score 664.4;  DB 6;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-189;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
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Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Qy        661 TCTTCC 666
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Db        661 TCTTCC 666


RESULT 3
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
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                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
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BASE COUNT      183 a    177 c    145 g    164 t
ORIGIN

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  Matches  659;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Db        181 ACTCTAGATTATATTCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
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Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
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Db        661 TCTTCC 666


RESULT 4
AR151062
LOCUS       AR151062                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
BASE COUNT      183 a    178 c    146 g    162 t
ORIGIN

  Query Match             96.9%;  Score 645.2;  DB 6;  Length 669;
  Best Local Similarity   98.0%;  Pred. No. 1.3e-183;
  Matches  653;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||| |
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        661 TCTTCC 666
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Db        661 TCTTCC 666
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RESULT 5
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  MEDLINE   98182592
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
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                     /db_xref="taxon:9685"
     CDS             1. .669
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                     /codon_start=1
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                     /db_xref="GI:2735053"
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                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
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                     LNSS"
BASE COUNT      191 a    179 c    137 g    162 t
ORIGIN

  Query Match           89.9%;  Score 598.8;  DB 4;  Length 669;
  Best Local Similarity   93.7%;  Pred. No. 1.4e-169;
  Matches  624;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  ||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||| ||||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666
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RESULT 6
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 13-MAY-1997
DEFINITION  F.catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      cat.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  MEDLINE   97246745
   PUBMED   9089110
FEATURES             Location/Qualifiers
     source          1. .669
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                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
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                     /product="interleukin-12 p35 chain"
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                     LNAS"
BASE COUNT      190 a    178 c    139 g    162 t
ORIGIN

  Query Match             89.9%;  Score 598.8;  DB 4;  Length 669;
  Best Local Similarity   93.7%;  Pred. No. 1.4e-169;
  Matches  624;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||||| |||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||||  || ||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||||| |||||||||| |||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
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Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 TCTTCC 666
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Db        661 GCTTCC 666
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RESULT 7
AX076201
LOCUS       AX076201                669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
BASE COUNT      189 a    179 c    140 g    161 t
ORIGIN

  Query Match             88.9%;  Score 592.4;  DB 6;  Length 669;
  Best Local Similarity   93.1%;  Pred. No. 1.2e-167;
  Matches  620;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  ||||||||||||||| |||||||||||||||||||||||||| ||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 TCTTCC 666
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Db        661 GCTTCC 666


RESULT 8
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
BASE COUNT      189 a    179 c    140 g    161 t
ORIGIN

  Query Match             88.9%;  Score 592.4;  DB 6;  Length 669;
  Best Local Similarity   93.1%;  Pred. No. 1.2e-167;
  Matches  620;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||| |||||||||| |||||||||||  ||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||| |||||||||||||||||||||||| ||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 TCTTCC 666
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Db        661 GCTTCC 666


RESULT 9
AX076477
LOCUS       AX076477                4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4201)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
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BASE COUNT     1086 a   1055 c    999 g   1061 t
ORIGIN

  Query Match             88.9%;  Score 592.4;  DB 6;  Length 4201;
  Best Local Similarity   93.1%;  Pred. No. 1.6e-167;
  Matches  620;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  |||||||||||||||||||||||||||||||||||||||| |||
Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||| |||||||||| |||||||||||  ||  ||||| |||||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||| |||||||||||||||||||||||| ||||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526
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Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||| ||||||||| | ||||||||||||||||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 3586

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3587 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 3646

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||| ||||| ||||||||| |||||||||||| |||||||||
Db       3647 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 3706

Qy        661 TCTTCC 666
              ||||||
Db       3707 GCTTCC 3712


RESULT 10
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

  Query Match             81.4%;  Score 542;  DB 6;  Length 660;
  Best Local Similarity   89.6%;  Pred. No. 2.1e-152;
  Matches  597;  Conservative    0;  Mismatches   60;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||||||||||||||||||||||||| | | |||||||||          |||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 51

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | ||||||     ||| | ||  ||||||||||  ||||  |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGC 111

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||||| ||||||||||||  ||| ||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAA 171

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||||  || ||||||||||||||||||||||||||||||||||||||||| |||
Db        172 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTA 291

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                |||||||||||  ||||| |||||||| ||||||||||| |||||  ||||| |||||
Db        292 AATTCCAGAGAGACTTCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCT 351

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||   |||||||||||||||| ||||||||||||||||||||||||||| ||||
Db        352 TTTATGACAACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| ||||||||| | ||| |||| ||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAA 471

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| ||||||||||||||||||||||||||||||||||| |||||||
Db        472 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || |||||||| |||||||||||| |||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        661 TCTTCC 666
              ||||||
Db        652 TCTTCC 657


RESULT 11
AX154621
LOCUS       AX154621                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

  Query Match             81.4%;  Score 542;  DB 6;  Length 660;
  Best Local Similarity   89.6%;  Pred. No. 2.1e-152;
  Matches  597;  Conservative    0;  Mismatches   60;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||||||||||||||||||||||||| | | |||||||||          |||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 51

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | ||||||     ||| | ||  ||||||||||  ||||  |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGC 111

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||||| ||||||||||||  ||| ||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAA 171

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||||  || ||||||||||||||||||||||||||||||||||||||||| |||
Db        172 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTA 291

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                |||||||||||  ||||| |||||||| ||||||||||| |||||  ||||| |||||
Db        292 AATTCCAGAGAGACTTCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCT 351

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||   |||||||||||||||| ||||||||||||||||||||||||||| ||||
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Db        352 TTTATGACAACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| |||||||| | ||| |||| ||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAA 471

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||||||||||||||||| |||||||
Db        472 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || |||||||| |||||||||||| |||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        661 TCTTCC 666
              ||||||
Db        652 TCTTCC 657


RESULT 12
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      184 a    172 c    141 g    163 t
ORIGIN

  Query Match             81.1%;  Score 540.4;  DB 6;  Length 660;
  Best Local Similarity   89.5%;  Pred. No. 6.4e-152;
  Matches  596;  Conservative    0;  Mismatches   61;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| |||||||||||||| | | |||||||||          |||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 51

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||| ||||  |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 111

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAA 171

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||| |||
Db        172 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||||||||||| ||| ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTG 291

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||| ||||||| |||||||||| |||||||||| |||||  ||||| |||||
Db        292 GCTTCCAGAGGGATCTCTCTGATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCT 351

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA.420
              |||||||||  |||||||||| |||| ||||||||||||||||||||||||||| ||||
Db        352 TTTATGACGACCCTGTGCCTTGGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| |||||||| | ||| |||| ||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAA 471

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||||||||||||||||| |||||||
Db        472 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || |||||||| |||||||||||| |||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        661 TCTTCC 666
              ||||||
Db        652 TCTTCC 657


RESULT 13
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    173 c    136 g    162 t
ORIGIN

  Query Match             81.1%;  Score 540.4;  DB 6;  Length 660;
  Best Local Similarity   89.5%;  Pred. No. 6.4e-152;
  Matches  596;  Conservative    0;  Mismatches   61;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||||||||||||||||||||||||| | | |||||||||          |||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 51

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | ||||||    ||| | ||  |||||||| ||||  |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGC 111

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAA 171

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||| |||
Db        172 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGACTGATCATGAAGATATCACAAAAGAT 231

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTA 291
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Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||  ||||| ||||||| |||||||||| |||||  ||||| |||||
Db        292 AATTCCAGAGAGACTTCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCT 351

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||   |||||||||||||||| ||||||||||||||||||||||||||||| ||||
Db        352 TTTATGACAACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| |||||||| | ||| |||| ||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAA 471

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||| |||||||||||||||||||||||||||||||||| |||||||
Db        472 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || ||||||||| |||||||||||| |||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        661 TCTTCC 666
              ||||||
Db        652 TCTTCC 657


RESULT 14
PIGIL12PSU
LOCUS       PIGIL12PSU              1426 bp    mRNA    linear   MAM 09-JUL-2001
DEFINITION  Sus scrofa interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   L35765
VERSION     L35765.1  GI:927204
KEYWORDS    .
SOURCE      Sus scrofa.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 1426)
  AUTHORS   Foss,D.L. and Murtaugh,M.P.
  TITLE     Molecular cloning and mRNA expression of porcine interleukin-12
  JOURNAL   Vet. Immunol. Immunopathol. 57 (1-2), 121-134 (1997)
  MEDLINE   97383978
   PUBMED   9239844
COMMENT     On Aug 2, 1995 this sequence version replaced gi:755667.
FEATURES             Location/Qualifiers
     source          1. .1426
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /cell_type="mononuclear"
                     /tissue_type="peripheral blood"
     CDS             108. .878
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAA73897.1"
                     /db_xref="GI:927205"
                     /translation="MCSPGFGLQTSDLTCDVHPSASSRRLAVTAAPLSMCPLRNLLLV
                     ATLVLLNHLDHLSLGRSLPATTAGPGMFKCLNHSQNLLKAVSNTLQKAKQTLEFYSCT
                     SEEIDHEDITKDKTSTVEACLPLELATNESCLAARETSLITNGNCLTSGKTSFMTTLC
                     LSSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQNMLTAITELMQALNFNSETVPQKP
                     SLEELDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS"
     primer_bind     196. .216
     primer_bind     complement(859. .878)
     polyA_site      1426
BASE COUNT      422 a    320 c    293 g    391 t
ORIGIN

  Query Match             81.0%;  Score 539.6;  DB 4;  Length 1426;
  Best Local Similarity   88.1%;  Pred. No. 1.2e-151;
  Matches  587;  Conservative    0;  Mismatches   79;  Indels    0;  Gaps    0;
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Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| |||| |||| |||||||||||| ||| |||||||| || | ||||||||||
Db        210 ATGTGTCCGCTGCGCAACCTCCTCCTTGTGGCCACCCTGGTCCTCCTCAACCACCTGGAC 269

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              || || | || || ||||||||||  || || || |  |||||||||| ||| | |||
Db        270 CATCTCAGTTTGGGCAGGAGCCTCCCTGCAACCACAGCAGGCCCAGGAATGTTCAAATGC 329

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| |||||||  |||||||||||| |||||||||||| ||||
Db        330 CTCAACCACTCCCAAAATCTGCTGAAGGCCGTCAGCAACACACTTCAGAAGGCCAAACAA 389

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              || |||||||| || |||||||||| |||||||| |||||||||||||||||| || |||
Db        390 ACCCTAGAATTTTACTCCTGCACTTCAGAAGAGATCGATCATGAAGATATCACCAAAGAT 449

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||| ||| || ||| ||||||||||||||||
Db        450 AAAACCAGCACAGTGGAGGCCTGCTTACCACTTGAACTAGCCACGAATGAGAGTTGCCTG 509

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||| ||||||||| |||||| |||||||| || | ||||||| | |||||||| |||||
Db        510 GCTGCCAGAGAGACCTCTTTAATAACTAATGGAAATTGCCTGACTTCTGGAAAGACCTCT 569

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||   |||||||||||||||| ||||| ||||||||||||||||||  ||||
Db        570 TTTATGACAACCCTGTGCCTTAGCAGTATCTACGAGGACTTGAAGATGTACCATGTGGAG 629

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||| |||||||||| |||||||| | |||||||| ||||||||||||||||||||||||
Db        630 TTCCAGGCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTGGATCAG 689

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||   ||||||| | ||||| |||||||||||||| |||||||
Db        690 AACATGCTGACAGCTATTACTGAGCTGATGCAGGCTCTGAATTTCAACAGTGAGACTGTG 749

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| ||||||| ||||| | |||||||||||| ||||||||||||||||||||||
Db        750 CCACAGAAGCCCTCCCTGGAAGAACTGGATTTTTATAAGACTAAAATCAAGCTCTGCATA 809

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||| |||||||||||||||||||||||| |||||||||| |||||||||
Db        810 CTTCTTCATGCCTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAAT 869

Qy        661 TCTTCC 666
              ||||||
Db        870 TCTTCC 875


RESULT 15
AX154619
LOCUS       AX154619                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 23 from Patent WO0140257.
ACCESSION   AX154619
VERSION     AX154619.1  GI:14536194
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      182 a    180 c    144 g    154 t
ORIGIN

  Query Match             80.7%;  Score 537.2;  DB 6;  Length 660;
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  Best Local Similarity   89.2%;  Pred. No. 5.9e-151;
  Matches  594;  Conservative    0;  Mismatches   63;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||| | | |||||||||         |||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 51

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||  |||||||||| |||| |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACCCCAGGCCCAGGAATGTTCCCATGC 111

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||| || |||||||||||||| |||||||||| ||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCTGTCAGCAACACGCTCCAGAAGGCCAAACAA 171

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              || |||||||| ||  ||||||||||||||||||||||||||||||||||||||||| |||
Db        172 ACCCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||||||||||| ||| ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTG 291

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||| |||||| |||||||||| |||||||||||||||  ||||| ||||
Db        292 GCTTCCAGAGGGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 351

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||   ||||||||||||||||||||||||||||||||||||||||||| ||||
Db        352 TTTATGACAACCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        412 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 471

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||||||| | |||||  | |||||||||||| |||||||| ||||| |
Db        472 AACATGCTGGCAGCTATTGCTGAGCTAATGCAGGCCCTGAATGTCAACAGTGAGACTGCG 531

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||| ||||| ||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || ||||||||| |||||||||||| |||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        661 TCTTCC 666
              ||||||
Db        652 TCTTCC 657


Search completed: July 16, 2003, 10:34:38
Job time : 1889.59 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 04:18:07 ; Search time 179.063 Seconds
(without alignments)
8375.975 Million cell updates/sec

Title: US-09-917-265-46
Perfect score: 666
Sequence: 1 atgtgcccgccgcgcggcct.....tgagttatctgaattcttcc 666

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	666	100.0	669	20	AAX35626	Nucleic acid encod
2	666	100.0	669	20	AAX03163	Nucleic acid encod
3	666	100.0	669	22	AAI64389	Canine coding sequ
4	666	100.0	1282	20	AAX18178	Canine full length
5	664.4	99.8	669	19	AAV13819	Canine IL-12 P35 s
6	645.2	96.9	669	19	AAV13818	Canine IL-12 P35 s
7	645.2	96.9	669	20	AAX35616	Nucleic acid encod
8	645.2	96.9	669	20	AAX03153	Nucleic acid encod
9	645.2	96.9	669	22	AAI64379	Canine coding sequ
10	598.8	89.9	1441	19	AAV56628	Feline FLAFp35 cDN
11	594	89.2	679	22	AAF26097	Feline fil12p35a D
12	592.4	88.9	669	22	AAF26083	Feline IL-12p35 en
13	592.4	88.9	669	22	AAF26086	Feline IL-12p35 en
14	592.4	88.9	4201	22	AAF26077	Feline IL-12p35 en
15	591	88.7	591	20	AAX18179	Canine mature CLAF
16	586	88.0	689	19	AAV56641	Feline FLAFp35 DNA
17	544.2	81.7	639	22	AAF26098	Plasmid pMOL-fIL12
18	542	81.4	660	22	AAD15213	Modified human cyt
19	542	81.4	660	22	AAD15220	Modified human cyt
20	540.4	81.1	660	22	AAD15216	Modified human cyt
21	540.4	81.1	660	22	AAD15217	Modified human cyt
22	537.2	80.7	660	22	AAD15218	Modified human cyt
23	535	80.3	591	19	AAV56629	Feline FLAFp35 cDN
24	530.8	79.7	660	22	AAD15219	Modified human cyt
25	529.2	79.5	660	22	AAD15214	Modified human cyt
26	529.2	79.5	660	22	AAD15215	Modified human cyt
27	528.4	79.3	666	22	AAD15211	Modified human cyt
28	522	78.4	666	22	AAD15212	Modified human cyt
29	518	77.8	660	16	AAQ97485	Human interleukin-
30	518	77.8	660	19	AAV07218	DNA encoding human
31	518	77.8	762	21	AAF21323	Human low adenosin
32	518	77.8	762	21	AAA35201	Human adenosine re
33	518	77.8	1364	17	AAT48099	Human interleukin-
34	518	77.8	1364	19	AAV42536	Human interleukin-
35	518	77.8	1364	19	AAV15228	Heterodimeric huma
36	518	77.8	1364	21	AAZ28863	Human interleukin-
37	518	77.8	1364	22	AAF56281	IL-12 vaccine adju
38	518	77.8	4521	21	AAF21326	Human low adenosin
39	518	77.8	4521	21	AAA35204	Human adenosine re
40	516.4	77.5	660	19	AAV07274	Human Interleukin-
41	516.4	77.5	660	20	AAZ40407	Human interleukin
42	516.4	77.5	762	20	AAV83207	Interleukin (IL)-1
43	516.4	77.5	1316	18	AAT63621	Interleukin-12 p35
44	516.4	77.5	1396	13	AAQ24371	Natural killer cel
45	516.4	77.5	5686	20	AAZ40415	Plasmid pIN1143 co

ALIGNMENTS

RESULT 1
AAX35626
ID AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC AAX35626;
XX
DT 09-JUL-1999 (first entry)
XX
DE Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1..669
FT /*tag= a
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR P-PSDB; AAY02343.

```
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match             100.0%;  Score 666;  DB 20;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-200;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 2
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match             100.0%;  Score 666;  DB 20;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-200;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666
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RESULT 3
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
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FT   sig_peptide     1..75
FT                   /*tag= b
FT   mat_peptide     76..666
FT                   /*tag= c
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PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;  99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Claim 6; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;
```

```
  Query Match             100.0%;  Score 666;  DB 22;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-200;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666
```

```
RESULT 4
AAX18178
ID   AAX18178 standard; cDNA; 1282 BP.
XX
```

```
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 other;

  Query Match            100.0%;  Score 666;  DB 20;  Length 1282;
  Best Local Similarity  100.0%;  Pred. No. 6.9e-200;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 125

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 185

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 245

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 305

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 365

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 425

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 485

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 545

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 605

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 665

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 725

Qy        661 TCTTCC 666
              ||||||
Db        726 TCTTCC 731


RESULT 5
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 11; Pages 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
```

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XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 other;

  Query Match            99.8%;  Score 664.4;  DB 19;  Length 669;
  Best Local Similarity  99.8%;  Pred. No. 1.6e-199;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 6
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match            96.9%;  Score 645.2;  DB 19;  Length 669;
  Best Local Similarity  98.0%;  Pred. No. 1.8e-193;
  Matches  653;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| |||||||||||||  | | ||||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||| |||||||||| ||||||| |
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 7
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             96.9%;  Score 645.2;  DB 20;  Length 669;
  Best Local Similarity   98.0%;  Pred. No. 1.8e-193;
  Matches  653;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||||  | | ||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||| |||||||||| ||||||| |
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 8
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
```

```
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             96.9%;  Score 645.2;  DB 20;  Length 669;
  Best Local Similarity   98.0%;  Pred. No. 1.8e-193;
  Matches  653;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||  | | ||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||.||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||| |
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 9
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1..75
FT                   /*tag=  b
FT   mat_peptide     76..666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             96.9%;  Score 645.2;  DB 22;  Length 669;
  Best Local Similarity   98.0%;  Pred. No. 1.8e-193;
  Matches  653;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||  | | ||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||| |||||||||| |||||||| |
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666
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RESULT 10
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133..811
FT                   /*tag= a
FT   sig_peptide     133..217
FT                   /*tag= b
FT   mat_peptide     218..808
FT                   /*tag= c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 other;
```

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  Query Match             89.9%;  Score 598.8;  DB 19;  Length 1441;
  Best Local Similarity   93.7%;  Pred. No. 1.3e-178;
  Matches  624;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||||||||| |||||||||||||| |||||||||||||| ||| |||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||||| |||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||||  || ||||||||||||||||||||||||||||||||||||||||| |||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||||| |||||||||  |||||||||||||||||  ||||| |||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||||| ||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| || ||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| || ||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 TCTTCC 666
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                ||||||
Db        803 TCTTCC 808


RESULT 11
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs -
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 other;

  Query Match             89.2%;  Score 594;  DB 22;  Length 679;
  Best Local Similarity   93.2%;  Pred. No. 2.9e-177;
  Matches  621;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||||||||| |||||||||||||| |||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| ||||||||| || |||| |||||||||| |||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| |||||| ||||| ||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  |||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||||| |||||||||| ||||||| |||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGGCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||| ||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||| ||||| | ||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAACCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||| |||||||| ||| | ||||||| ||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAAAGTGATGAGCTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 12
AAF26083
ID   AAF26083 standard; DNA; 669 BP.
XX
AC   AAF26083;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
```

```
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter -
XX
PS   Claim 14; Page 37; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 other;

  Query Match             88.9%;  Score 592.4;  DB 22;  Length 669;
  Best Local Similarity   93.1%;  Pred. No. 9.2e-177;
  Matches  620;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| ||||||||| || |||| |||||||||| |||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  |||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||||| |||||||||| |||||||||||||  ||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||||| ||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| ||||||||| | ||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||| ||||| |||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 TCTTCC 666
                |||||
Db        661 GCTTCC 666


RESULT 13
AAF26086
ID   AAF26086 standard; DNA; 669 BP.
XX
AC   AAF26086;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs -
XX
PS   Claim 3; Page 31; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 other;

  Query Match             88.9%;  Score 592.4;  DB 22;  Length 669;
```

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  Best Local Similarity   93.1%;  Pred. No. 9.2e-177;
  Matches  620;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||| |||||||||||||| |||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  |||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||||| |||||||||| |||||||||||||  ||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  ||||||||||||||| ||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||||| ||||||||| | ||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||| ||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 GCTTCC 666


RESULT 14
AAF26077
ID   AAF26077 standard; DNA; 4201 BP.
XX
AC   AAF26077;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter  -
XX
PS   Disclosure; Page 31-33; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 other;

  Query Match           88.9%;  Score 592.4;  DB 22;  Length 4201;
  Best Local Similarity   93.1%;  Pred. No. 2.5e-176;
  Matches  620;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||||||||| |||||||||||||| |||||||||||||| ||| ||||||||||
Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  |||||||||||||||||||||||||||||||||||||||||| |||
Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||||| |||||||||| |||||||||||||  ||  ||||| |||||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  ||||||||||||||| ||||||||||||||||||||||||||| ||||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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                ||||||||||||||||| ||||||||| | ||||||||||||||||||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 3586

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                ||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3587 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 3646

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
                |||||||||||||||||||| ||||| ||||||||| |||||||||||| |||||||||
Db       3647 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 3706

Qy        661 TCTTCC 666
                ||||||
Db       3707 GCTTCC 3712


RESULT 15
AAX18179
ID   AAX18179 standard; cDNA; 591 BP.
XX
AC   AAX18179;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74325.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 34-35; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 other;

  Query Match             88.7%;  Score 591;  DB 20;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-176;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Qy         136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy         196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy         256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Qy         376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy         436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy         496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy         556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy         616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591


Search completed: July 16, 2003, 06:46:40
Job time : 181.063 secs
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:30:08 ; Search time 1206.92 Seconds
(without alignments)
8936.974 Million cell updates/sec

Title: US-09-917-265-46
Perfect score: 666
Sequence: 1 atgtgcccgccgcgcggcct.....tgagttatctgaattcttcc 666

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	253.2	38.0	812	12	BG702253	BG702253 602683459
	2	227.2	34.1	589	9	AI050362	AI050362 ub30a07.r
c	3	210.2	31.6	1099	13	BI523344	BI523344 603175938
	4	188.8	28.3	373	12	BF552757	BF552757 UI-R-C0-i
	5	187	28.1	832	13	BI523569	BI523569 603175938
	6	138.8	20.8	342	13	BM257856	BM257856 521721 MA
	7	72.8	10.9	447	13	BI824638	BI824638 603033580
c	8	56.2	8.4	528	9	AI332701	AI332701 qq19a07.x
	9	44	6.6	939	17	CNS00CNG	AL059400 Drosophil
	10	41.6	6.2	569	13	BI765729	BI765729 603046443
	11	41.6	6.2	599	12	BG714277	BG714277 602674965
	12	40.2	6.0	787	17	CNS010B7	AL098749 Drosophil
	13	39.2	5.9	912	12	BG770771	BG770771 602740813
	14	39	5.9	1042	17	CNS00BVZ	AL057907 Drosophil
	15	38.6	5.8	602	13	BM577222	BM577222 170006871
	16	38.2	5.7	579	9	AL783454	AL783454 AL783454
	17	38.2	5.7	906	10	BE537025	BE537025 601063459
	18	37.8	5.7	976	12	BE871124	BE871124 601447380
	19	37.2	5.6	407	14	T44964	T44964 8227 Lambda
	20	37.2	5.6	462	14	H76322	H76322 18027 Lambd
c	21	37	5.6	438	10	AW389687	AW389687 RC3-ST016
	22	36.8	5.5	726	17	CNS04HZF	AL291588 Tetraodon
	23	36.8	5.5	1038	17	AQ900448	AQ900448 HS_2072_B
	24	36.6	5.5	532	13	BI065861	BI065861 pgf1n.pk0
	25	36.6	5.5	583	13	BJ305783	BJ305783 BJ305783
	26	36.6	5.5	612	10	AV827486	AV827486 AV827486
c	27	36.6	5.5	617	13	BJ311377	BJ311377 BJ311377
	28	36.6	5.5	644	10	AV825194	AV825194 AV825194
	29	36.6	5.5	652	10	AV823245	AV823245 AV823245
	30	36.6	5.5	678	13	BJ317111	BJ317111 BJ317111
c	31	36.6	5.5	692	13	BJ322650	BJ322650 BJ322650
c	32	36.6	5.5	693	10	AV784178	AV784178 AV784178
	33	36.2	5.4	292	12	BF116640	BF116640 uy99h04.y
	34	36.2	5.4	390	10	AW631037	AW631037 hh91b12.y
	35	36.2	5.4	484	14	T22900	T22900 4908 Lambda
	36	36.2	5.4	492	10	AW369275	AW369275 QV1-BN000
	37	36.2	5.4	628	13	BM011789	BM011789 603636162
	38	36.2	5.4	648	12	BG898673	BG898673 HOA3-1-H-
	39	36.2	5.4	707	13	BM046186	BM046186 603625949
	40	36.2	5.4	713	14	BM828150	BM828150 K-EST0100
	41	36.2	5.4	777	9	AU130730	AU130730 AU130730
	42	36.2	5.4	836	13	BI116347	BI116347 602869091
	43	36.2	5.4	1029	12	BE869200	BE869200 601445006
c	44	36	5.4	633	12	BE973158	BE973158 601652043
	45	35.8	5.4	181	9	AI938452	AI938452 sc45e07.y

ALIGNMENTS

RESULT 1
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.
FEATURES Location/Qualifiers

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    source          1. .812
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:4816118"
                    /clone_lib="NIH_MGC_95"
                    /tissue_type="hippocampus"
                    /lab_host="DH10B"
                    /note="Organ: brain; Vector: pBluescriptR (modified
                    pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                    ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                    size-selected for  average insert size 2.5 kb and
                    normalized to ROT 5. This is a primary library enriched
                    for  full-length clones and constructed using the
                    Cap-trapper method (Carninci, in preparation).  Library
                    constructed by M. Brownstein (NIMH/NHGRI, National
                    Institutes of Health).  Note: this is a NIH_MGC Library."
BASE COUNT      188 a    249 c    226 g    149 t
ORIGIN

  Query Match             38.0%;  Score 253.2;  DB 12;  Length 812;
  Best Local Similarity   81.6%;  Pred. No. 7.3e-64;
  Matches  333;  Conservative    0;  Mismatches   63;  Indels   12;  Gaps    3;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||||| | | |||||||||          |||||||
Db        417 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 467

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||||| ||||  |||
Db        468 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 527

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        528 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 587

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| |||||||| ||||||||||||||||||| |||
Db        588 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGAT 647

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||| |||||||||||| ||||||||||||
Db        648 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGC--T 705

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||  |||||| |||||||| |||||||||||||  |||  ||||| |||||
Db        706 AAATCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGG-CTCCAGAAAGACCTCT 764

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATG 408
              |||||||  |||||||||||| || ||    ||   |  ||||||
Db        765 TTTATGATGTGCCTGTGCCTTAGTAGTATTATGAAGACTTGAAAGATG 812


RESULT 2
AI050362
LOCUS       AI050362                589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES              Location/Qualifiers
     source           1. .589
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:1379220"
                      /clone_lib="Soares_thymus_2NbMT"
                      /sex="male"
                      /tissue_type="Thymus"
                      /dev_stage="4 weeks"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTT
                      3']; double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. RNA
                      provided by Dr. Bertrand Jordan. Library went through two
                      rounds of normalization, and was constructed by Bento
                      Soares and M.Fatima Bonaldo."
BASE COUNT      162 a    159 c    142 g    126 t
ORIGIN

  Query Match             34.1%;  Score 227.2;  DB 9;  Length 589;
  Best Local Similarity   73.0%;  Pred. No. 3.2e-56;
  Matches  292;  Conservative    0;  Mismatches  108;  Indels    0;  Gaps    0;

Qy        170 AGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATA 229
              |||||||| ||| || ||   |||||||||| | ||||| || |||||||||| |
Db        109 AGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGACA 168

Qy        230 TCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATG 289
              |||||  |||  |||||||||||| || || |||| |||||||||||| ||  || ||| |
Db        169 TCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAACG 228

Qy        290 AGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTG 349
              |||||||||||||| | |||||||  ||||  | ||| |  |||||| ||||||  || |
Db        229 AGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCAC 288

Qy        350 GAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGT 409
              ||| | ||||| |||| |  |||||||||| | ||||||||||||||||||||||||||
Db        289 AGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGT 348

Qy        410 ACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCT 469
              ||||||  || ||| ||||||| ||||||   |||   |   |   | |   |||||||
Db        349 ACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATCA 408

Qy        470 TTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACA 529
              |||| ||  |   |||||||   |  |||||||||||| | ||| | ||||||   ||
Db        409 TTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTGATGCAGTCTCTGAATCATAATG 468

Qy        530 GTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGA 569
              | | |||| |||  |||||| |  ||  ||  |||  | |
Db        469 GCGAGACTCTGCGCCAGAAACCTCCCTGTGGGGAGAAGCA 508


RESULT 3
BI523344/c
LOCUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
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DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      359 a    244 c    218 g    276 t      2 others
ORIGIN

  Query Match           31.6%;  Score 210.2;  DB 13;  Length 1099;
  Best Local Similarity   87.7%;  Pred. No. 4.6e-51;
  Matches  264;  Conservative    0;  Mismatches   33;  Indels    4;  Gaps    3;

Qy        369 GGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGC 428
              || ||||||| |||| || || ||||| ||| |||||||||||||| |||| |||||| |
Db        741 GGCCCTGTGCTTTAGTAGTATTTATGAAGAC-TGAAGATGTACCAGGTGGAGTTCAAGAC 683

Qy        429 CATGAACGCAAAGCTT-TTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGC 487
              |||||| |||||||||  | |||||||| |||||||||||||||| ||||||||||||
Db        682 CATGAATGCAAAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGC 623

Qy        488 TGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGA 547
              || ||| ||| ||||||||| | |||||||||||||||||||| |||||||||||| |
Db        622 TGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAA 563

Qy        548 AATCCTCCCTTGAAGAGCCGGAT--TTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 605
              |||||||||||||||| ||||||  |||   |||||| ||||||||||||||||||||||
Db        562 AATCCTCCCTTGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCT 503

Qy        606 TCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTC 665
              |||||||||||||||||| || ||||| || |||||| ||||||| ||||||||| ||||
Db        502 TCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTC 443

Qy        666 C 666
              |
Db        442 C 442
```

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RESULT 4
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /clone_lib="UI-R-C0"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0
                     library is a subtracted library derived from the UI-R-A1
                     and UI-R-E1 libraries. The UI-R-A1 library consisted of a
                     mixture of individually tagged normalized libraries
                     constructed from rat  placenta, adult lung, brain, liver,
                     kidney, heart, spleen, ovary,  and muscle. The UI-R-E1
                     library  consisted of a mixture of individually tagged
                     normalized libraries constructed from 8, 12 and 18-day
                     embryo. The tag is a string of 3-5 nucleotides present
                     between the Not I  site and the oligo-dT track which
                     allows identification of the library of origin of a clone
                     within the mixture. The subtracted library (UI-R-C0) was
                     constructed as follows: PCR amplified cDNA inserts from a
                     pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
                     been derived was used as a driver in a hybridization with
                     the pooled UI-R-A1 and UI-R-E1 library in the form of
                     single-stranded circles.  The remaining single-stranded
                     circles (subtracted library) was purified by
                     hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (Life Technologies) to generate the UI-R-C0
                     library. This procedure has been previously described
                     (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                     1996)"
BASE COUNT      106 a     93 c     89 g     85 t
ORIGIN

  Query Match           28.3%;  Score 188.8;  DB 12;  Length 373;
  Best Local Similarity   69.6%;  Pred. No. 6.4e-45;
  Matches  256;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;
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Qy        291 GAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGG 350
              ||| |||||||||| | | |||||  ||||  ||||  |  ||||| ||||||  |  |
Db          4 GAGGTGCCTGGCTACTAAAGAGACTTCTTCCATAATAAGAGGGAGCTGCCTGCCTCCACA 63

Qy        351 AAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTA 410
              |||| | |||||  |||| |  ||||||||||  | ||||||||||||||||||||||||
Db         64 AAAGACTTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGTA 123

Qy        411 CCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTT 470
              ||||   || ||| |||||||  || |||   |||   |   |     |   |||||||
Db        124 CCAGTCAGAGTTCCAGGCCATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCAC 183

Qy        471 TCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAG 530
              ||||||   ||||||||||  |||||  ||||||||  | | | | ||||||  || | |
Db        184 TCTGGACAGAAACATGCTGATGGCTATTGATGAGCTAATGCGGTCTCTGAATCACAGCGG 243

Qy        531 TGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAA 590
              | || | |||  |||||| |  || | | |||  | |||  ||| | |   || || ||
Db        244 CGAGATTCTGCACCAGAAAGCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAA 303

Qy        591 GCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAG 650
              |||||| || || || ||||| |||||  |  || |   |||| ||| | ||  ||||||
Db        304 GCTCTGTATCCTGCTCCATGCCTTCAGCACACGCGTCATGACTATCAACAGGGTGATGAA 363

Qy        651 TTATCTGA 658
              ||||||||
Db        364 CTATCTGA 371
```

```
RESULT 5
BI523569
LOCUS       BI523569                 832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 23
            High quality sequence stop: 821.
FEATURES             Location/Qualifiers
     source          1. .832
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      220 a    233 c    200 g    179 t
ORIGIN
```

```
  Query Match             28.1%;  Score 187;  DB 13;  Length 832;
  Best Local Similarity   81.4%;  Pred. No. 3.1e-44;
  Matches  232;  Conservative    0;  Mismatches   45;  Indels    8;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| |||||||||||||| | | |||||||| ||   ||||||
Db        321 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTCCTGGACCACCTCAGT 380

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
                  |||| |  | | |||||||   ||| | ||   ||||||||| ||||  |||
Db        381 --------TTGGCCATGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 432

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        433 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 492

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| |||||||||||||||||||||||||||||| |||
Db        493 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 552

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285
              |||||||||||||||||||||| |||||| |||||||||||| |
Db        553 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 597
```

```
RESULT 6
BM257856
LOCUS       BM257856                 342 bp    mRNA    linear   EST 17-DEC-2001
DEFINITION  521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BM257856
VERSION     BM257856.1  GI:17893455
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 125  row: E  column: 18
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .342
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 3BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
```

Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
BASE COUNT 67 a 135 c 74 g 66 t
ORIGIN

Query Match 20.8%; Score 138.8; DB 13; Length 342;
Best Local Similarity 81.3%; Pred. No. 4e-30;
Matches 174; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

```
Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||||| ||| ||||||||||  |  ||| |||||| || ||   ||||||| |
Db        132 ATGTGCCCGCTTCGCAGCCTCCTCCTCATATCCACCCTGGTTCTCCTCCACCACCTGCCC 191

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || || ||||||||||||||  || || | ||||||||||    |   |||
Db        192 CACCTCAGTTTGGGCAGGAGCCTCCCCACCACCACAGCAAGCCCAGGAAGGAGC---TGC 248

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||| || ||||||||||||||||| || ||||||||||||| ||||||||||||||||||
Db        249 CTCGACTACTCCCAAAACCTGCTGAGGGCTGTCAGCAACACGCTACAGAAGGCCAGACAA 308

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGA 214
              |||||||||| || |||||||||| || ||||
Db        309 ACTCTAGAATTTTACTCCTGCACTTCTGAGGAGA 342
```

RESULT 7
BI824638
LOCUS BI824638 447 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5', mRNA sequence.
ACCESSION BI824638
VERSION BI824638.1 GI:15936188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11435 row: o column: 19
High quality sequence start: 3
High quality sequence stop: 445.
FEATURES Location/Qualifiers
source 1. .447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5175018"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
BASE COUNT 149 a 63 c 87 g 148 t
ORIGIN

Query Match 10.9%; Score 72.8; DB 13; Length 447;
Best Local Similarity 91.7%; Pred. No. 1.6e-10;
Matches 77; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy        583 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGA 642
              ||||||||||||||||||||||||||||||||||||||||||||| || ||||| || ||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGA 60

Qy        643 ATGATGAGTTATCTGAATTCTTCC 666
              ||||||| ||||||||| |||||
Db         61 GTGATGAGCTATCTGAATGCTTCC 84
```

RESULT 8
AI332701/c
LOCUS AI332701 528 bp mRNA linear EST 13-FEB-1999
DEFINITION qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948 3' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI332701
VERSION AI332701.1 GI:4069260
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1469 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
FEATURES Location/Qualifiers
source 1. .528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1932948"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
BASE COUNT 189 a 93 c 63 g 183 t
ORIGIN

Query Match 8.4%; Score 56.2; DB 9; Length 528;
Best Local Similarity 88.4%; Pred. No. 1.5e-05;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy        598 ATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTG 657
              |||||||| ||||||||||||||||| || ||||| || |||||| ||||||| |||||||
Db        528 ATACTTCTCCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTG 469

Qy        658 AATTCTTCC 666
              ||| |||||
Db        468 AATTCTTCC 460
```

```
Db        468 AATGCTTCC 460


RESULT 9
CNS00CNG
LOCUS       CNS00CNG                939 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR26H16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL059400
VERSION     AL059400.1  GI:4946964
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .939
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="BACR26H16"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
BASE COUNT       71 a    349 c    104 g    180 t    235 others
ORIGIN

  Query Match             6.6%;  Score 44;  DB 17;  Length 939;
  Best Local Similarity   15.7%;  Pred. No. 0.077;
  Matches   42;  Conservative  120;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          4 TGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGACCAC 63
              | ||| || : :  || :| |||| |  ||||||    |||      ||:||:   || |
Db        297 TCCCCCCCAYYYMCCCMMCCCCTTCTYCCCATCCMMCCCCTCTCCCCCCMCCYATCCCTC 356

Qy         64 CTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTC 123
              :  :::|   :|     |: :::|::  |: :::: : ::::  :  :  :::   ::|:
Db        357 MMMMYHTTYMMCCCCCCCMCMMMCHMTCCMMMMMMMMMMMMMMMMTMHMMMMMMMMMTM 416

Qy        124 AACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACT 183
              ::::::| :::|: ::     : : ::     : :::: :  :: ::  ::: :::: :
Db        417 MHMMMMTTMMHAMTMMCMTMTMMMMMMMMTTMMTMMMMMMMMMMMMMMTMMMMMMMTMM 476

Qy        184 CTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAA 243
              : : ::|:: :  ::  :::| :: :: : : : :::  :: :|: : ::::  : :::
Db        477 MMMMMMTHMMHMMMMMMHHMTMMMMMHMMMMMHTHHMMMMMMMMTMMMTMMMMMMMMMM 536

Qy        244 ACCAGCACAGTGGAGGCCTGCTTACCAC 271
                ::: ::::    :  ::: :  ::|::
Db        537 TMMMMHMMMMMMMMMMHHMMMMMMCMM 564
```

```
RESULT 10
BI765729
LOCUS       BI765729                569 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603046443F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186675 5',
            mRNA sequence.
ACCESSION   BI765729
VERSION     BI765729.1  GI:15757307
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc..
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11466  row: e  column: 12
            High quality sequence start: 35
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5186675"
                     /clone_lib="NIH_MGC_116"
                     /lab_host="DH10B"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
BASE COUNT      112 a    171 c    182 g    104 t
ORIGIN

  Query Match             6.2%;  Score 41.6;  DB 13;  Length 569;
  Best Local Similarity   57.8%;  Pred. No. 0.32;
  Matches   74;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         69 TTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCA 128
              | | ||||| ||   |||| | ||| | ||  |||||||  ||  ||| |   ||  |||
Db        283 TGGAGCCAGAAGTGGCCCCTCTGCCCCTCCAGGCCCAGGCATGGTCCTGCTGCTTCACCC 342

Qy        129 CTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGA 188
              |||||  | ||||| | | | |     | ||| |||   ||    ||| |    | | ||
Db        343 CTCCCCTAGCCTGCCGTGTGGCACTGCCCACAGGCTGGGGACAAGCAGCCCTTGTGTTGA 402

Qy        189 ATTATATT 196
                | |  ||
Db        403 GTCAGGTT 410


RESULT 11
BG714277
LOCUS       BG714277                599 bp    mRNA    linear   EST 08-MAY-2001
DEFINITION  602674965F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797232 5',
            mRNA sequence.
ACCESSION   BG714277
VERSION     BG714277.1  GI:13993208
```

```
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10683  row: b  column: 17
            High quality sequence stop: 586.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4797232"
                     /clone_lib="NIH_MGC_96"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length  clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      146 a    171 c    183 g     99 t
ORIGIN

  Query Match             6.2%;  Score 41.6;  DB 12;  Length 599;
  Best Local Similarity   57.8%;  Pred. No. 0.33;
  Matches   74;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         69 TTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCA 128
              | | ||||| ||   |||| | ||| | ||  |||||||  ||  ||| |   ||  |||
Db        248 TGGAGCCAGAAGTGGCCCCTCTGCCCCTCCAGGCCCAGGCATGGTCCTGCTGCTTCACCC 307

Qy        129 CTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGA 188
              |||||  | ||||| | | | |     | ||| ||||   ||    ||| |    | | ||
Db        308 CTCCCCTAGCCTGCCGTGTGGCACTGCCCACAGGCTGGGGACAAGCAGCCCTTGTGTTGA 367

Qy        189 ATTATATT 196
              | |  ||
Db        368 GTCAGGTT 375


RESULT 12
CNS010B7
LOCUS       CNS010B7                787 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN03M07 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL098749
VERSION     AL098749.1  GI:5610360
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .787
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="BACN03M07"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
BASE COUNT       52 a    114 c     73 g     19 t    529 others
ORIGIN

  Query Match             6.0%;  Score 40.2;  DB 17;  Length 787;
  Best Local Similarity   3.8%;  Pred. No. 0.96;
  Matches   15;  Conservative  122;  Mismatches  257;  Indels    0;  Gaps    0;

Qy         15 CGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGC 74
              |    :| || :  |     :||   :  :  : ::  :      :   :::: ::
Db        362 CNCNNKCNTCTKNNTNNKKNKCCNNCKNNKNNKNMKKNMNNMNNKMNKNMKKMNNKKNNN 421

Qy         75 CAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCA 134
              : ::  ::    : :: :  :  : :  :         ::   ::      :    : :
Db        422 MNKKNTMMMNNKMCMMNMKMMNKMNMMNMKNMMNNNNKKNNKKKMNNNNNMNNKNMMNMN 481

Qy        135 AAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATA 194
              :   ::::: :   ::          :::  : : :    :  ::::::  :
Db        482 NNMKNNNMKKMKNMMNTNNMKNTNNNNMNNNMMKNKKNMNMMNNNKMNNNKMKMMKMMM 541

Qy        195 TTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGT 254
              :     :  :   ::   : :: :        ::   : :    : ::  : : : ::
Db        542 NKNNMMNTMNNMKNNMKNNKKNKMMMKNNNTMNAMKNKKMKMNNNNMNMMKNMNMKNKK 601

Qy        255 GGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGAT 314
              :: ::|:   :   :  :        :  ::        :  ::   :
Db        602 NNNNMNMKNMKTMNNNMNNNMNNKNNNNNNNNMMCMKKNNNCTKNMKNNKMNNNMMKNNN 661

Qy        315 CTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCT 374
              : :|     : ::|     : :  :|   ::  |       ::      : :       |
Db        662 MMMTMNNNCMNMKANTMMNMNKMMMCMNNMMNNTNMKNNNNMMNNMMNNMKNNNMMNKT 721

Qy        375 GTGCCTTAGCAGCATCTATGAGGACTTGAAGATG 408
              :|: :|:    :   :  :  ::    : :::
Db        722 NKGMNKTMNKCNMNNNMMMNMNNMMNNNNMNMKK 755


RESULT 13
BG770771
LOCUS       BG770771                912 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602740813F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4870730 5',
            mRNA sequence.
ACCESSION   BG770771
VERSION     BG770771.1  GI:14081424
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
```

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1744  row: i  column: 03
            High quality sequence start: 66
            High quality sequence stop: 503.
FEATURES             Location/Qualifiers
     source          1. .912
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4870730"
                     /clone_lib="NIH_MGC_49"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library. |"
BASE COUNT      218 a    344 c    237 g    112 t      1 others
ORIGIN

  Query Match             5.9%;  Score 39.2;  DB 12;  Length 912;
  Best Local Similarity   48.2%;  Pred. No. 2;
  Matches  110;  Conservative    0;  Mismatches  118;  Indels    0;  Gaps    0;

Qy        368 CGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGG 427
              ||| | || |||| | || | |  | ||||| ||| | |||| ||   ||||  |||
Db        138 CGGCCGTGCGCCTCATCACCCTGGAGGAGGAGATGACCAAGTACAAGCCCGAATCGGAGG 197

Qy        428 CCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGC 487
                 |||  ||| ||    | |  ||   |       |   || |   ||   ||| || ||
Db        198 AGCTGACGGCAGAGAGGATCACAGAGTTCTGCCACCGCTTCCTGGAGGGCAAAATCAAGC 257

Qy        488 TGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGA 547
                      ||     |||||    ||| |  | |      |   ||| |  ||||
Db        258 CCCACCTGATGAGCCAGCTGCCGGAGGACTGGGACAAGCAGCCTGTCAAGGTGCTTGTTG 317

Qy        548 AATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCT 595
                  | | |||||   || |||| |    || | ||  ||  |||
Db        318 GGAAGAACTTCGAAGACGTGGCTTTTGACTGCACGACAAAAAACGTCT 365


RESULT 14
CNS00BVZ
LOCUS       CNS00BVZ                1042 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR24D11 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL057907
VERSION     AL057907.1  GI:4938170
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1042)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1042
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="BACR24D11"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
BASE COUNT      296 a    126 c     92 g    220 t    308 others
ORIGIN

  Query Match             5.9%;  Score 39;  DB 17;  Length 1042;
  Best Local Similarity   27.7%;  Pred. No. 2.4;
  Matches   74;  Conservative   43;  Mismatches  150;  Indels    0;  Gaps    0;

Qy        360 TTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGA 419
              ||| ||:|       :    |    |          | :   | | :| :  ::  |
Db        452 TTTNATSANANNAANSNNAATNNTNAAATAAANNAANSNTNTNASSAASNTSSNAAANNT 511

Qy        420 ATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCA 479
              ||   |::         | |     ||       :  ||     | |             |
Db        512 NTTTSNGSSNSNTNTNANATAAAAAATANANANNSNNAAANAAAAAAANAANNNNNNNA 571

Qy        480 AAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGT 539
              ||| |       |        | |   :|||:     :| |:|| : |:::||:: :||
Db        572 AAANAAAAANSAAAASTNANNTTANNARTTASTAATTSTTAWTTSBTASWKTGWKTSTGA 631

Qy        540 GCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCAT 599
              :  | ||| ||: |: : |:||    :  : ||  ||: || ||  || | ::::
Db        632 KAGAGAGATATSTTSTSATSAATSTTSATWSTTSSATVTAAATASTATTATSMWSAAATS 691

Qy        600 ACTTCTTCATGCTTTCAGAATTCGTGC 626
              |:||::|:||   :|:  | | :: ::
Db        692 ASTTSYTSATATSWTSTAATTSSSSSS 718


RESULT 15
BM577222
LOCUS       BM577222                602 bp    mRNA    linear   EST 22-FEB-2002
DEFINITION  17000687163491 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
            19600449712899 5', mRNA sequence.
ACCESSION   BM577222
VERSION     BM577222.1  GI:18865689
KEYWORDS    EST.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
            ,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
  TITLE     Celera Anopheles gambiae EST project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Holt R.A.
            Celera Genomics
            45 w. Gude Dr., Rockville, MD 20850, USA
            Tel: 2404533151
            Fax: 2404534580
```

```
           Email: HoltRA@celera.com
           Plate: NU01004AWU  row: B  column: 21
           Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Anopheles gambiae"
                     /strain="RSP-ST (Reduced susc. to Permethrin - std.
                     chromosome)"
                     /db_xref="taxon:7165"
                     /clone="19600449712899"
                     /clone_lib="A.Gam.ad.cDNA.blood1"
                     /dev_stage="Adult"
                     /lab_host="DH10b"
                     /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole
                     adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
                     hours  after human blood feeding. cDNA inserts >500 bp
                     cloned directionally  into pSport 1. Not 1 site is 3'.
                     Clones available through the Malaria  Research and
                     Reference Reagent Resource Center (www.malaria.mr4.org)"
BASE COUNT      201 a    124 c    149 g    128 t
ORIGIN

  Query Match             5.8%;  Score 38.6;  DB 13;  Length 602;
  Best Local Similarity   52.9%;  Pred. No. 2.5;
  Matches   83;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        392 ATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGG 451
              | ||||| ||   ||||||| | | | |||| |||   || ||||||  |  || |   |
Db        151 AGGAGGATTTACGGATGTACGAAACGCAATTGAAGCTAATCAACGCAGAAATTATGGAGT 210

Qy        452 ATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTAC 511
              ||    ||  | ||| | |  | |||  || | ||  |   | |      ||   |||
Db        211 ATGTGCAGTTGAAGAACATGATCGATACAATCTTGGGGCAGGATCGACGCGAAGAGTTCA 270

Qy        512 AGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAA 548
              || | | |     || | ||| ||   ||     |||
Db        271 AGACGCAGGTCAACATCGGTGGGAACATGTTCATGAA 307


Search completed: July 16, 2003, 13:00:34
Job time : 1212.92 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 06:24:59 ; Search time 36.7239 Seconds
(without alignments)
5561.687 Million cell updates/sec

Title: US-09-917-265-46
Perfect score: 666
Sequence: 1 atgtgcccgccgcgcggcct.....tgagttatctgaattcttcc 666

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	664.4	99.8	669	4	US-09-079-984A-12	Sequence 12, Appl
	2	645.2	96.9	669	4	US-09-079-984A-2	Sequence 2, Appli
	3	518	77.8	660	1	US-08-186-529-3	Sequence 3, Appli
	4	518	77.8	660	1	US-08-640-386A-3	Sequence 3, Appli
	5	518	77.8	1364	1	US-08-265-087-3	Sequence 3, Appli
	6	518	77.8	1364	1	US-08-621-493-3	Sequence 3, Appli
	7	518	77.8	1364	2	US-08-965-688-3	Sequence 3, Appli
	8	518	77.8	1364	4	US-09-260-173-3	Sequence 3, Appli
	9	516.4	77.5	762	4	US-08-848-760B-21	Sequence 21, Appl
	10	516.4	77.5	1316	2	US-08-684-687-3	Sequence 3, Appli
	11	516.4	77.5	1316	4	US-09-851-520-3	Sequence 3, Appli
	12	514.8	77.3	721	2	US-08-184-009-199	Sequence 199, App
	13	514.8	77.3	721	2	US-08-458-356-199	Sequence 199, App
	14	514.8	77.3	721	4	US-08-460-736-199	Sequence 199, App
	15	514.8	77.3	1026	2	US-08-751-767A-1	Sequence 1, Appli
	16	514.8	77.3	1645	4	US-09-310-842-2	Sequence 2, Appli
	17	484.8	72.8	1560	2	US-08-751-767A-11	Sequence 11, Appl
	18	484.8	72.8	1623	2	US-08-751-767A-9	Sequence 9, Appli
	19	484.8	72.8	6139	2	US-08-751-767A-7	Sequence 7, Appli
	20	303.2	45.5	713	2	US-08-385-335A-10	Sequence 10, Appl
	21	220.6	33.1	6295	2	US-08-659-206A-4	Sequence 4, Appli
	22	220.6	33.1	7287	2	US-08-659-206A-1	Sequence 1, Appli
	23	33.6	5.0	1545	1	US-07-872-673B-2	Sequence 2, Appli
	24	33.6	5.0	1696	4	US-09-198-603C-3	Sequence 3, Appli
	25	33.6	5.0	2454	1	US-07-872-673B-1	Sequence 1, Appli
c	26	32.4	4.9	3124	4	US-09-734-030-1	Sequence 1, Appli
c	27	32.4	4.9	7542	4	US-09-734-030-3	Sequence 3, Appli
c	28	32	4.8	7425	4	US-09-453-702B-212	Sequence 212, App
	29	31.4	4.7	4031	1	US-08-159-784-1	Sequence 1, Appli
c	30	31.2	4.7	39	4	US-09-079-984A-6	Sequence 6, Appli
c	31	31.2	4.7	489	1	US-07-879-685B-3	Sequence 3, Appli
c	32	31.2	4.7	8438	1	US-07-945-283-1	Sequence 1, Appli
	33	31.2	4.7	169998	4	US-09-676-610B-24	Sequence 24, Appl
c	34	31	4.7	12886	4	US-09-453-702B-14	Sequence 14, Appl
c	35	30.8	4.6	2824	2	US-09-010-928B-3	Sequence 3, Appli
c	36	30.8	4.6	13953	4	US-09-738-884-3	Sequence 3, Appli
	37	30.2	4.5	3900	2	US-08-356-060A-42	Sequence 42, Appl
	38	30.2	4.5	3900	4	US-08-460-900C-42	Sequence 42, Appl
	39	30.2	4.5	3900	4	US-08-674-509B-42	Sequence 42, Appl
	40	30.2	4.5	3900	4	US-08-954-698-42	Sequence 42, Appl
	41	30.2	4.5	3900	4	US-08-957-874-42	Sequence 42, Appl
	42	30.2	4.5	4434	2	US-08-540-406-5	Sequence 5, Appli
	43	30.2	4.5	4434	3	US-08-656-055-5	Sequence 5, Appli
	44	30.2	4.5	4434	4	US-08-954-668-5	Sequence 5, Appli
	45	30.2	4.5	4434	4	US-08-918-658-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT 1
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-12

  Query Match             99.8%;  Score 664.4;  DB 4;  Length 669;
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  Best Local Similarity   99.8%;  Pred. No. 5.4e-206;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 2
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

  Query Match             96.9%;  Score 645.2;  DB 4;  Length 669;
  Best Local Similarity   98.0%;  Pred. No. 9.2e-200;
  Matches  653;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| |||||||||||||  | | ||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        661 TCTTCC 666
                ||||||
Db        661 TCTTCC 666


RESULT 3
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-186-529-3

  Query Match             77.8%;  Score 518;  DB 1;  Length 660;
  Best Local Similarity   87.4%;  Pred. No. 1.9e-158;
  Matches  582;  Conservative    0;  Mismatches   75;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||  ||  |||||  |||||||||||||| | | |||||||||          |||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 51

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||  | ||  ||||||  | |||||||   |||  | ||   |||||||||  ||||  |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 111

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  ||||||||||||||||||||  ||||||||||||  |||  ||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 171

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||  ||  | ||||||||  ||||||||||||||||||||||||||||| |||
Db        172 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||  ||||||  ||||||||||||  ||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 291

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                ||||||||||||  ||||||  ||||||||  ||||||||||||||||||  |||||  |||||
Db        292 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 351

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| ||  ||||||||||||  ||  ||  |||||  ||||||||||||||||||  ||||
Db        352 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 411

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||  ||||||  ||||||||  | ||||||||  ||||||||||||||||||  ||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 471

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||  |||  |||  |||||||||  | ||||||||||||||||||||||  |||||||
Db        472 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||  ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||  ||  |||||  ||  ||||||  |||||||  |||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 651

Qy        661 TCTTCC 666
                |||||
Db        652 GCTTCC 657


RESULT 4
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
```

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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

  Query Match             77.8%;  Score 518;  DB 1;  Length 660;
  Best Local Similarity   87.4%;  Pred. No. 1.9e-158;
  Matches  582;  Conservative    0;  Mismatches   75;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||| | | |||||||||          |||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 51

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||| |||| |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 111

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  ||||||||||||||||||||| |||||||||||| ||| ||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 171

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||||  ||  | |||||||| ||||||||||||||||||||||||||| |||
Db        172 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 291

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||| |||||| |||||||| ||||||||||||||||  ||||| |||||
Db        292 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 351

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| ||||||||||||||||||| ||||
Db        352 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 411

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| ||||||||| | |||||||| |||||||||||||||||| ||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 471

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| |||||||| | |||||||||||||||||||||| |||||||
Db        472 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || ||||| || |||||| ||||||| |||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 651

Qy        661 TCTTCC 666
              ||||||
Db        652 GCTTCC 657


RESULT 5
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-265-087-3

  Query Match             77.8%;  Score 518;  DB 1;  Length 1364;
  Best Local Similarity   87.4%;  Pred. No. 2.9e-158;
  Matches  582;  Conservative    0;  Mismatches   75;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||| | | |||||||||          |||||||
Db        203 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 253

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||| |||| |||
Db        254 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 313

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  ||||||||||||||||||||| |||||||||||| ||| ||||||||||||||
Db        314 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 373

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||||  ||  | |||||||| ||||||||||||||||||||||||||| |||
Db        374 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 433

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||
Db        434 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 493

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||| |||||| |||||||| ||||||||||||||||  ||||| |||||
Db        494 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 553

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| ||||||||||||||||||| ||||
Db        554 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 613
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Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| |||||||| | |||||||| |||||||||||||||| ||||||
Db        614 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 673

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| ||||||||| | ||||||||||||||||||||| |||||||
Db        674 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 733

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        734 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 793

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || ||||| || |||||| ||||||| |||||||||
Db        794 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 853

Qy        661 TCTTCC 666
              ||||||
Db        854 GCTTCC 859


RESULT 6
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

  Query Match             77.8%;  Score 518;  DB 1;  Length 1364;
  Best Local Similarity   87.4%;  Pred. No. 2.9e-158;

  Matches  582;  Conservative    0;  Mismatches   75;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| |||||||||||||| | | |||||||||          |||||||
Db        203 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 253

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||||| ||||  |||
Db        254 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 313

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  ||||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        314 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 373

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| |||||||||||||||||||||||||||| |||
Db        374 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 433

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||| |||||||||| ||||||||||||||||||
Db        434 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 493

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||| |||||| |||||||| |||||||||||||||  ||||| |||||
Db        494 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 553

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| |||||||||||||||||| ||||
Db        554 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 613

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| |||||| ||||||||| | |||||||| |||||||||||||||| ||||||
Db        614 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 673

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| ||||||||| | |||||||||||||||||||| |||||||
Db        674 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 733

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        734 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 793

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || ||||| || |||||| ||||||| |||||||||
Db        794 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 853

Qy        661 TCTTCC 666
              ||||||
Db        854 GCTTCC 859


RESULT 7
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3

  Query Match             77.8%;  Score 518;  DB 2;  Length 1364;
  Best Local Similarity   87.4%;  Pred. No. 2.9e-158;
  Matches  582;  Conservative    0;  Mismatches   75;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||||| | | |||||||||          |||||||
Db        203 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 253

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||| |||| |||
Db        254 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 313

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||||| |||||||||||| ||| ||||||||||||||
Db        314 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 373

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| ||||||||||||||||||||||||||| |||
Db        374 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 433

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||| |||||| |||||||||||| ||||||||||||||
Db        434 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 493

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||| |||||| |||||||| |||||||||||||||||  ||||| |||||
Db        494 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 553

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| |||||||||||||||||| ||||
Db        554 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 613

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| ||||||||| | |||||||| ||||||||||||||||| ||||||
Db        614 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 673

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| ||||||||| | |||||||||||||||||||| |||||||
Db        674 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 733

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        734 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 793

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||| || ||||| || |||||| ||||||| |||||||||
Db        794 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 853

Qy        661 TCTTCC 666
              ||||||
Db        854 GCTTCC 859


RESULT 8
US-09-260-173-3
; Sequence 3, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
;             STREET: Spring House Corporate Center, PO Box 457
;             CITY: Spring House
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/260,173
;             FILING DATE: 01-Mar-1999
;             CLASSIFICATION: <Unknown>
;                             17-JUN-1994
;                             18-APR-1994
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/965,688
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/265,087
;             FILING DATE: 17-JUN-1994
;             APPLICATION NUMBER: US 08/229,282
;             FILING DATE: 18-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: WST51AUSA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-540-9206
;             TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1364 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  101..859
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

  Query Match             77.8%;  Score 518;  DB 4;  Length 1364;
  Best Local Similarity   87.4%;  Pred. No. 2.9e-158;
  Matches  582;  Conservative    0;  Mismatches   75;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||||| | | |||||||||          |||||||
Db        203 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 253
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Qy          61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
               ||||| | || |||||| | |||||||   ||| | ||   |||||||||| |||| |||
Db         254 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 313

Qy         121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
               ||  |||||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db         314 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 373

Qy         181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
               |||||||||| ||  | |||||||| ||||||||||||||||||||||||||||| |||
Db         374 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 433

Qy         241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
               |||||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||
Db         434 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 493

Qy         301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                 |||||||||| |||||| |||||||| ||||||||||||||||  ||||| |||||
Db         494 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 553

Qy         361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
               ||||||| || |||||||||||| || || ||||| |||||||||||||||||| ||||
Db         554 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 613

Qy         421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
               |||||| ||||||| ||||||||| | |||||||| |||||||||||||||||| ||||||
Db         614 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 673

Qy         481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
               ||||||||| ||| ||| ||||||||| | |||||||||||||||||||| ||||||
Db         674 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 733

Qy         541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
               ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         734 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 793

Qy         601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
               ||||||||||||||||||||||| || ||||| || |||||| |||||| |||||||||
Db         794 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 853

Qy         661 TCTTCC 666
                 ||||||
Db         854 GCTTCC 859


RESULT 9
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-848-760B-21

  Query Match             77.5%;  Score 516.4;  DB 4;  Length 762;
  Best Local Similarity   87.2%;  Pred. No. 6.9e-158;
  Matches  581;  Conservative    0;  Mismatches   76;  Indels    9;  Gaps    1;

Qy           1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
               ||||| ||  ||||| |||||||||||||  | | |||||||||          |||||||
Db         103 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCT---------CCTGGAC 153

Qy          61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
               ||||| | || |||||| | |||||||   ||| | ||   |||||||||| |||| |||
Db         154 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 213

Qy         121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
               ||  |||||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db         214 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 273

Qy         181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
               |||||||||| ||  | |||||||| ||||||||||||||||||||||||||||| |||
Db         274 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 333

Qy         241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
               |||||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||
Db         334 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 393

Qy         301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                 |||||||||| |||||| |||||||| ||||||||||||||||  ||||| |||||
Db         394 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 453

Qy         361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
               ||||||| || |||||||||||| || || ||||| |||||||||||||||||| ||||
Db         454 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 513

Qy         421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
               |||||| ||||||| ||||||||| | |||||||| |||||||||||||||||| ||||||
Db         514 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 573

Qy         481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
               ||||||||| ||| ||| ||||||||| | |||||||||||||||||||| ||||||
Db         574 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 633

Qy         541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
               ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         634 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 693

Qy         601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
               ||||||||||||||||||||||| || ||||| || |||||| |||||| |||||||||
Db         694 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 753

Qy         661 TCTTCC 666
                 ||||||
Db         754 GCTTCC 759


RESULT 10
US-08-684-687-3
; Sequence 3, Application US/08684687
```

```
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  102..863
US-08-684-687-3

  Query Match             77.5%;  Score 516.4;  DB 2;  Length 1316;
  Best Local Similarity   87.2%;  Pred. No. 9.5e-158;
  Matches  581;  Conservative    0;  Mismatches   76;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| |||||||||||||  | | |||||||||         |||||||
Db        204 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCT---------CCTGGAC 254

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||||| ||||  |||
Db        255 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 314

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        315 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 374

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| ||||||||||||||||||||||||||||| |||
Db        375 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 434

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||||
Db        435 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 494

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||| |||||| |||||||| ||||||||||||||||||  ||||| |||||
Db        495 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 554

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| ||||||||||||||||||| ||||
Db        555 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 614

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| ||||||||| | |||||||| |||||||||||||||| ||||||
Db        615 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 674

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| |||||||| | ||||||||||||||||||||| ||||||
Db        675 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 734

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        735 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 794

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || ||||| || |||||| ||||||| |||||||||
Db        795 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 854

Qy        661 TCTTCC 666
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Db        855 GCTTCC 860


RESULT 11
US-09-851-520-3
; Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

  Query Match             77.5%;  Score 516.4;  DB 4;  Length 1316;
  Best Local Similarity   87.2%;  Pred. No. 9.5e-158;
  Matches  581;  Conservative    0;  Mismatches   76;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| |||||||||||||  | | |||||||||         |||||||
Db        204 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCT---------CCTGGAC 254

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||||| ||||  |||
Db        255 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 314

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        315 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 374

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| ||||||||||||||||||||||||||||| |||
Db        375 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 434

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||||
Db        435 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 494
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Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||| |||||| ||||||| ||||||||||||||||  ||||| |||||
Db        495 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 554

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| ||||||||||||||||||  ||||
Db        555 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 614

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| ||||||||| | |||||||| |||||||||||||||||  ||||||
Db        615 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 674

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| |||||||||| | ||||||||||||||||||||||| |||||||
Db        675 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 734

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        735 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 794

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||| || ||||| || |||||| ||||||| |||||||||
Db        795 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 854

Qy        661 TCTTCC 666
              ||||||
Db        855 GCTTCC 860


RESULT 12
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-199
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  Query Match           77.3%;  Score 514.8;  DB 2;  Length 721;
  Best Local Similarity  87.1%;  Pred. No. 2.2e-157;
  Matches  580;  Conservative    0;  Mismatches   77;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| |||||||||||||| | | |||||||||          |||||||
Db         62 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 112

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   ||||||||| ||||  |||
Db        113 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 172

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        173 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 232

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| ||||||||||||||||||||||||||||||| |||
Db        233 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 292

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||
Db        293 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 352

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||| |||||| |||||||| |||||||||||||||  ||||| |||||
Db        353 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 412

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| ||||||||||||||||||  ||||
Db        413 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 472

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| ||||||||| | |||||||| |||||||||||||||||  ||||||
Db        473 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 532

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| |||||||||| | ||||||||||||||||||||||| |||||||
Db        533 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 592

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        593 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 652

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||| || ||||| || || ||| ||| ||| |||||||||
Db        653 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAAT 712

Qy        661 TCTTCC 666
              |||||
Db        713 GCTTCC 718


RESULT 13
US-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/458,356
;       FILING DATE:  02-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/184,009
;       FILING DATE:  19-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Frommer, William S.
;       REGISTRATION NUMBER:  25,506
;       REFERENCE/DOCKET NUMBER:  454310-2530
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 840-3333
;       TELEFAX:  (212) 840-0712
;       TELEX:  425066CURTMS
;   INFORMATION FOR SEQ ID NO:  199:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  721 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-458-356-199

  Query Match             77.3%;  Score 514.8;  DB 2;  Length 721;
  Best Local Similarity   87.1%;  Pred. No. 2.2e-157;
  Matches  580;  Conservative    0;  Mismatches   77;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||||| | | |||||||||         |||||||
Db         62 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 112

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||| |||| |||
Db        113 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 172

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||| |||||||||||| ||| ||||||||||||||
Db        173 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 232

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| |||||||||||||||||||||||||||| |||
Db        233 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 292

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||
Db        293 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 352

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||| |||||| |||||||| |||||||||||||||  ||||| |||||
Db        353 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 412

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| |||||||||||||||||| ||||
Db        413 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 472

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| ||||||||| | |||||||| |||||||||||||||| ||||||
Db        473 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 532

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| |||||||| | ||||||||||||||||||||| |||||||
Db        533 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 592

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        593 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 652

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||| || ||||| || || ||| ||| ||| |||||||||
Db        653 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAAT 712

Qy        661 TCTTCC 666
              ||||||
Db        713 GCTTCC 718


RESULT 14
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

  Query Match             77.3%;  Score 514.8;  DB 4;  Length 721;
  Best Local Similarity   87.1%;  Pred. No. 2.2e-157;
  Matches  580;  Conservative    0;  Mismatches   77;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  ||||| ||||||||||||||| | | |||||||||         |||||||
Db         62 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 112

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||| |||| |||
Db        113 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 172

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||| |||||||||||| ||| ||||||||||||||
Db        173 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 232

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| ||  | |||||||| |||||||||||||||||||||||||||| |||
Db        233 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 292

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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                    |||||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||||
Db        293 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 352

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                |||||||||||| |||||| |||||||| ||||||||||||||||  ||||| |||||
Db        353 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 412

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
                ||||||| || |||||||||||| || || ||||| ||||||||||||||||||| ||||
Db        413 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 472

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
                |||||| |||||| | ||||||||| | |||||||| |||||||||||||||||| ||||||
Db        473 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 532

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
                ||||||||| ||| ||| ||||||||| | |||||||||||||||||||| |||||||
Db        533 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 592

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        593 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 652

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
                |||||||||||||||||||||| || ||||| || || ||| ||| ||| |||||||||
Db        653 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAAT 712

Qy        661 TCTTCC 666
                ||||||
Db        713 GCTTCC 718


RESULT 15
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  170..826
US-08-751-767A-1

  Query Match             77.3%;  Score 514.8;  DB 2;  Length 1026;
  Best Local Similarity   87.1%;  Pred. No. 2.7e-157;
  Matches  580;  Conservative    0;  Mismatches   77;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||| ||  |||||||||||||||| | | |||||||||          |||||||
Db        170 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 220

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||| | |||||||   ||| | ||   |||||||||| ||||  |||
Db        221 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 280

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||||||||||||| |||||||||||| ||| ||||||||||||||||
Db        281 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 340

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||||  ||  | |||||||| ||||||||||||||||||||||||||||| |||
Db        341 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 400

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||||
Db        401 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 460

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||| |||||| |||||||| ||||||||||||||||  ||||| |||||
Db        461 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 520

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||| || |||||||||||| || || ||||| |||||||||||||||||| ||||
Db        521 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 580

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||| ||||||| ||||||||| | |||||||| |||||||||||||||||| ||||||
Db        581 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 640

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||| ||| ||| ||||||||| | |||||||||||||||||||| |||||||
Db        641 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 700

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Qy        661 TCTTCC 666
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Db        821 GCTTCC 826


Search completed: July 16, 2003, 13:21:03
Job time : 38.7239 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:38:23 ; Search time 130.328 Seconds
(without alignments)
8158.492 Million cell updates/sec

Title: US-09-917-265-46
Perfect score: 666
Sequence: 1 atgtgcccgccgcgcggcct.....tgagttatctgaattcttcc 666

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1114047 seqs, 798260406 residues

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	666	100.0	666	10	US-09-917-265-46	Sequence 46, Appl
c 2	666	100.0	666	10	US-09-917-265-48	Sequence 48, Appl
3	666	100.0	1455	10	US-09-917-265-104	Sequence 104, App
c 4	666	100.0	1455	10	US-09-917-265-106	Sequence 106, App
5	600.4	90.2	666	10	US-09-917-265-32	Sequence 32, Appl
c 6	600.4	90.2	666	10	US-09-917-265-34	Sequence 34, Appl
7	598.8	89.9	1441	12	US-10-079-616-8	Sequence 8, Appli
8	591	88.7	591	10	US-09-917-265-49	Sequence 49, Appl
c 9	591	88.7	591	10	US-09-917-265-51	Sequence 51, Appl
10	586	88.0	689	12	US-10-079-616-26	Sequence 26, Appl
11	543.4	81.6	1533	10	US-09-917-265-66	Sequence 66, Appl
c 12	543.4	81.6	1533	10	US-09-917-265-68	Sequence 68, Appl
13	543.4	81.6	1599	10	US-09-917-265-61	Sequence 61, Appl
c 14	543.4	81.6	1599	10	US-09-917-265-63	Sequence 63, Appl
15	535	80.3	591	10	US-09-917-265-35	Sequence 35, Appl
c 16	535	80.3	591	10	US-09-917-265-37	Sequence 37, Appl
17	535	80.3	591	12	US-10-079-616-9	Sequence 9, Appli
18	518	77.8	1395	10	US-09-924-703-5	Sequence 5, Appli
19	517.8	77.7	1533	10	US-09-917-265-43	Sequence 43, Appl
c 20	517.8	77.7	1533	10	US-09-917-265-45	Sequence 45, Appl
21	517.8	77.7	1599	10	US-09-917-265-38	Sequence 38, Appl
c 22	517.8	77.7	1599	10	US-09-917-265-40	Sequence 40, Appl
23	516.4	77.5	660	10	US-09-754-014-6	Sequence 6, Appli
24	516.4	77.5	660	10	US-09-836-866-4	Sequence 4, Appli
25	516.4	77.5	762	9	US-09-826-025-21	Sequence 21, Appl
26	514.8	77.3	1026	9	US-10-172-399-5	Sequence 5, Appli
27	514.8	77.3	1645	9	US-10-228-811-2	Sequence 2, Appli
28	511.4	76.8	561	10	US-09-917-265-101	Sequence 101, App
c 29	511.4	76.8	561	10	US-09-917-265-103	Sequence 103, App
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33	487	73.1	8623	10	US-09-828-825-5	Sequence 5, Appli
34	487	73.1	8629	10	US-09-828-825-15	Sequence 15, Appl
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36	487	73.1	8644	10	US-09-828-825-13	Sequence 13, Appl
37	487	73.1	8659	10	US-09-828-825-11	Sequence 11, Appl
38	371.8	55.8	660	10	US-09-754-014-8	Sequence 8, Appli
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41	71	10.7	79	12	US-10-079-616-24	Sequence 24, Appl
42	56.2	8.4	95	12	US-10-079-616-22	Sequence 22, Appl
43	37.8	5.7	1316	10	US-09-070-927A-191	Sequence 191, App
44	36.2	5.4	445	9	US-09-918-995-35388	Sequence 35388, A
45	36.2	5.4	6577	10	US-09-880-107-2187	Sequence 2187, Ap

ALIGNMENTS

RESULT 1
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION:
US-09-917-265-46

Query Match 100.0%; Score 666; DB 10; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.6e-211;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

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Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
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Db        661 TCTTCC 666
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RESULT 2
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-48

  Query Match           100.0%;  Score 666;  DB 10;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-211;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

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Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
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Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Qy        661 TCTTCC 666
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Db          6 TCTTCC 1
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RESULT 3
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
;   OTHER INFORMATION:
US-09-917-265-104

  Query Match           100.0%;  Score 666;  DB 10;  Length 1455;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-211;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        232 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 291

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Db        292 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 351
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Db        412 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 471

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        472 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 531

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        532 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 591

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 651

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
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Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Qy        661 TCTTCC 666
              ||||||
Db        892 TCTTCC 897
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RESULT 4
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-106

Query Match 100.0%; Score 666; DB 10; Length 1455;
Best Local Similarity 100.0%; Pred. No. 2.6e-211;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 1045

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 985

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        924 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 865

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
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Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 745

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 685

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 625

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 565

Qy        661 TCTTCC 666
              ||||||
Db        564 TCTTCC 559
```

RESULT 5
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION:
US-09-917-265-32

Query Match 90.2%; Score 600.4; DB 10; Length 666;
Best Local Similarity 93.8%; Pred. No. 1.3e-189;
Matches 625; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
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                  |||||||||||||||| |||||||||||||||| |||||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
                  ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
                  |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
                  |||||||||| || ||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                  |||||||||||||||| |||||||||| ||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
                  |||||||||  |||||||||||||||| |||||||||||||||||||||||||| ||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
                  |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
                  |||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                  |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
                  |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 TCTTCC 666
                  ||||||
Db        661 GCTTCC 666
```

RESULT 6
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-34

Query Match 90.2%; Score 600.4; DB 10; Length 666;
Best Local Similarity 93.8%; Pred. No. 1.3e-189;
Matches 625; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||||||||||| |||||||||||||||| |||||||||||||||| ||| ||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||| |||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||| |||||||||| ||||||||||||||||  ||||| |||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||||| ||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||| |||||||||  |||||||||||||  |||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 TCTTCC 666
              ||||||
Db          6 GCTTCC 1
```

RESULT 7
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. US20020107366A1
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1441 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             89.9%;  Score 598.8;  DB 12;  Length 1441;
  Best Local Similarity   93.7%;  Pred. No. 7e-189;
  Matches  624;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||| ||| ||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||| |||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              |||||||||||||||| ||||||||| |||||||||||||||  ||||| |||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||| |||||||||||||||||||||||| ||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||  |||||||| ||||| || ||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||| ||||||||| |||||||||||| || ||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 TCTTCC 666
              ||||||
Db        803 TCTTCC 808


RESULT 8
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-49

  Query Match             88.7%;  Score 591;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-186;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Qy        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591


RESULT 9
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

  Query Match           88.7%;  Score 591;  DB 10;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-186;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 532

Qy        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 472

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 292

Qy        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 232

Qy        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 112

Qy        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 1


RESULT 10
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match           88.0%;  Score 586;  DB 12;  Length 689;
  Best Local Similarity  92.5%;  Pred. No. 8.2e-185;
  Matches  616;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              |||||||| || || |||||||||| |||||||||||||||||| | |||||||||
Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||| | || |||||||| ||||||||| || |||| |||||||||| |||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||| |||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| | ||||||||| | ||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306
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Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||| |||||||||| ||||||||||||||||||  ||||| |||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              |||||||||  |||||||||||||||| ||||||||||||||||||||||||||| ||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| | |||||||| || ||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||| ||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| || |||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| || ||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        661 TCTTCC 666
              ||||||
Db        667 TCTTCC 672
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RESULT 11
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-66

Query Match 81.6%; Score 543.4; DB 10; Length 1533;
Best Local Similarity 94.8%; Pred. No. 2.2e-170;
Matches 562; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Qy         74 CCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCC 133
              | || | | | || ||  |  | ||   ||| || || ||||| ||  | ||||||||||
Db        941 CTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCC 1000

Qy        134 AAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTAT 193
              ||| | || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 AAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTAT 1060

Qy        194 ATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAG 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 ATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAG 1120

Qy        254 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 1180

Qy        314 TCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 TCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCC 1240

Qy        374 TGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGA 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 TGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGA 1300

Qy        434 ACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 ACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 1360

Qy        494 CTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCT 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 CTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCT 1420

Qy        554 CCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1421 CCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 1480

Qy        614 TCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
              |||||||||||||||||||||||| ||||||||||   ||  |||| ||||||
Db       1481 TCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533
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RESULT 12
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-68

Query Match 81.6%; Score 543.4; DB 10; Length 1533;
Best Local Similarity 94.8%; Pred. No. 2.2e-170;
Matches 562; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Qy         74 CCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCC 133
              | || | | | || ||  |  | ||   ||| || || ||||| ||  | ||||||||||
Db        593 CTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCC 534

Qy        134 AAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTAT 193
              ||| | || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTAT 474

Qy        194 ATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAG 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAG 414

Qy        254 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 354

Qy        314 TCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCC 294

Qy        374 TGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGA 433
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Db        293 TGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGA 234

Qy        434 ACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 174

Qy        494 CTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCT 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 CTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCT 114

Qy        554 CCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 CCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 54

Qy        614 TCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
              |||||||||||||||||||| |||||||||||   ||  |||| ||||||
Db         53 TCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 13
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match            81.6%;  Score 543.4;  DB 10;  Length 1599;
  Best Local Similarity  94.8%;  Pred. No. 2.3e-170;
  Matches  562;  Conservative    0;  Mismatches   31;  Indels    0;  Gaps    0;

Qy         74 CCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCC 133
              | || | | | || ||  |  | ||   ||| || || ||||| ||  | ||||||||||
Db       1007 CTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCC 1066

Qy        134 AAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTAT 193
              ||| | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1067 AAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTAT 1126

Qy        194 ATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAG 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1127 ATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAG 1186

Qy        254 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1187 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 1246

Qy        314 TCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1247 TCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCC 1306

Qy        374 TGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGA 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1307 TGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGA 1366

Qy        434 ACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 ACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 1426

Qy        494 CTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCT 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1427 CTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCT 1486

Qy        554 CCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1487 CCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 1546

Qy        614 TCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
              |||||||||||||||||||| |||||||||||   ||  |||| ||||||
Db       1547 TCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 14
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match            81.6%;  Score 543.4;  DB 10;  Length 1599;
  Best Local Similarity  94.8%;  Pred. No. 2.3e-170;
  Matches  562;  Conservative    0;  Mismatches   31;  Indels    0;  Gaps    0;

Qy         74 CCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCC 133
              | || | | | || ||  |  | ||   ||| || || ||||| ||  | ||||||||||
Db       593 CTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCC 534

Qy        134 AAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTAT 193
              ||| | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       533 AAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTAT 474

Qy        194 ATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAG 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       473 ATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAG 414

Qy        254 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       413 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 354

Qy        314 TCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       353 TCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCC 294

Qy        374 TGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGA 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       293 TGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGA 234

Qy        434 ACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       233 ACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 174

Qy        494 CTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCT 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       173 CTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCT 114
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Qy        554 CCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 CCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 54

Qy        614 TCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
              |||||||||||||||||||||| ||||||||||    ||  |||| ||||||
Db         53 TCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 15
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-35

  Query Match             80.3%;  Score 535;  DB 10;  Length 591;
  Best Local Similarity   94.1%;  Pred. No. 7.8e-168;
  Matches  556;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135
              |||| |||||||||| || |||| |||||||||| ||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195
              | |||||| |||| |||||||||||||||||||||||||||||||||||||||||| ||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375
              ||| |||||||||| ||||||||||||||||  ||||| ||||||||||||||  ||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435
              |||||||||| ||||||||||||||||||||||||| |||| ||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
              || ||||||||||||||||||||||| |||||||||||||||||||||||| ||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
               | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
              |||||||||||| ||||||||| |||||||||||||| ||||||||| |||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


Search completed: July 16, 2003, 13:16:25
Job time : 131.328 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:54:38 ; Search time 22.3163 Seconds
(without alignments)
1325.559 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1128	100.0	222	19	AAW41793	Canine IL-12 P35 s
2	1128	100.0	222	20	AAY02343	Canine Interleukin
3	1128	100.0	222	20	AAW74324	Canine full length
4	1128	100.0	222	20	AAW84374	Canine interleukin
5	1128	100.0	222	22	AAG66483	Canine protein #4.
6	1099	97.4	222	19	AAW41792	Canine IL-12 P35 s
7	1099	97.4	222	20	AAY02340	Canine Interleukin
8	1099	97.4	222	20	AAW84372	Canine interleukin
9	1099	97.4	222	22	AAG66481	Canine protein #2.
10	1046	92.7	222	19	AAW76175	Feline FLAFp35 pro
11	994	88.1	197	20	AAW74325	Canine mature CLAF
12	967.5	85.8	219	22	AAE08606	Modified human cyt
13	967.5	85.8	219	22	AAE08613	Modified human cyt
14	962.5	85.3	219	22	AAE08610	Modified human cyt
15	958.5	85.0	219	22	AAE08609	Modified human cyt
16	957.5	84.9	219	22	AAE08611	Modified human cyt
17	948.5	84.1	219	22	AAE08612	Modified human cyt
18	940.5	83.4	219	16	AAR79187	Human interleukin-
19	940.5	83.4	219	19	AAW51222	Human interleukin-
20	940.5	83.4	253	17	AAW07399	Human interleukin-
21	940.5	83.4	253	18	AAW09780	Interleukin-12 p35
22	940.5	83.4	253	19	AAW62993	Human interleukin-
23	940.5	83.4	253	19	AAW44325	Heterodimeric huma
24	940.5	83.4	253	21	AAY44182	Human interleukin-
25	940.5	83.4	253	22	AAB67263	IL-12 vaccine adju
26	936.5	83.0	219	22	AAE08608	Modified human cyt
27	935.5	82.9	253	13	AAR23729	Natural killer cel
28	934.5	82.8	219	18	AAW24236	35 kDa subunit of
29	934.5	82.8	219	18	AAW36940	35 kDa subunit of
30	934.5	82.8	219	18	AAW36942	35 kDa subunit of
31	934.5	82.8	219	19	AAW58726	Cytotoxic lymphocy
32	934.5	82.8	219	19	AAW51312	Human Interleukin-
33	934.5	82.8	219	19	AAW57483	Human interleukin-
34	934.5	82.8	219	20	AAY42488	Human interleukin
35	934.5	82.8	219	21	AAB23795	Human interleukin
36	934.5	82.8	219	21	AAY54918	Human p35 protein
37	934.5	82.8	219	22	AAE08614	Human cytokine p35
38	933.5	82.8	219	22	AAE08607	Modified human cyt
39	932	82.6	197	19	AAW76176	Feline FLAFp35 mat
40	930.5	82.5	219	12	AAR12494	Cytotoxic lymphocy
41	926.5	82.1	221	22	AAE08604	Modified human cyt
42	914.5	81.1	221	22	AAE08605	Modified human cyt
43	900.5	79.8	221	18	AAW08482	Sequence of ovine
44	876.5	77.7	527	23	AAE19817	Human IL-12.1 prot
45	875.5	77.6	537	23	AAE19820	Human IL-12.2 prot

ALIGNMENTS

RESULT 1
AAW41793
ID AAW41793 standard; peptide; 222 AA.
XX
AC AAW41793;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P35 subunit.
XX
KW Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW antiviral; vaccine adjuvant.
XX
OS Canis sp.
XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.
DR N-PSDB; AAV13819.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT activities are expected
XX

PS Claim 3; Pages 11-12; 12pp; Japanese.
XX
CC The present sequence is a canine interleukin-12 (IL-12) P35
CC subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antivirus and
CC vaccine adjuvant activities are expected.
XX
SQ Sequence 222 AA;

Query Match 100.0%; Score 1128; DB 19; Length 222;
Best Local Similarity 100.0%; Pred. No. 2e-106;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
Db 1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy 61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
Db 61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy 121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
Db 121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy 181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
Db 181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222

RESULT 2
AAY02343
ID AAY02343 standard; Protein; 222 AA.
XX
AC AAY02343;
XX
DT 09-JUL-1999 (first entry)
XX
DE Canine Interleukin-12 (IL-12) protein sequence.
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease.
XX
OS Canis sp.
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR N-PSDB; AAX35626.
XX
PT A prevention and treating agent containing interleukin 12 (CaIL12) -
PT for prevention and treatment of dog and cat immune diseases
XX
PS Claim 1; Page 15-16; 16pp; Japanese.
XX
CC The present sequence represents canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
SQ Sequence 222 AA;

Query Match 100.0%; Score 1128; DB 20; Length 222;
Best Local Similarity 100.0%; Pred. No. 2e-106;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
Db 1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy 61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
Db 61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy 121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
Db 121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy 181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
Db 181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222

RESULT 3
AAW74324
ID AAW74324 standard; Protein; 222 AA.
XX
AC AAW74324;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine full length CLAF p35 subunit.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP02295.
XX
PR 03-JUN-1997; 97JP-0161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Eda Y, Imamura T, Maeda H, Tokiyoshi S;
XX
DR WPI; 1999-070260/06.
DR N-PSDB; AAX18178.
XX
PT Canine cytokine protein which activates canine cytotoxic T
PT lymphocytes - is useful for treatment of viral and autoimmune
PT diseases in dogs
XX
PS Claim 1; Page 26-28; 51pp; Japanese.
XX
CC This sequence is the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs.
XX

```
SQ   Sequence   222 AA;

  Query Match           100.0%;  Score 1128;  DB 20;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 2e-106;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222


RESULT 4
AAW84374
ID   AAW84374 standard; Protein; 222 AA.
XX
AC   AAW84374;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03163.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   222 AA;

  Query Match           100.0%;  Score 1128;  DB 20;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 2e-106;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222


RESULT 5
AAG66483
ID   AAG66483 standard; Protein; 222 AA.
XX
AC   AAG66483;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..25
FT                   /label= Signal_peptide
FT   Protein         26..222
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64389.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
```

```
XX
SQ   Sequence   222 AA;

  Query Match             100.0%;  Score 1128;  DB 22;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 2e-106;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222


RESULT 6
AAW41792
ID   AAW41792 standard; peptide; 222 AA.
XX
AC   AAW41792;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant.
XX
OS   Canis sp.
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   N-PSDB; AAV13818.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 3; Page 9; 12pp; Japanese.
XX
CC   The present sequence is a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence   222 AA;

  Query Match             97.4%;  Score 1099;  DB 19;  Length 222;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-103;
  Matches  217;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MCPARSLLLVATLVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
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Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLSSS 222
              |||||||||||||||||||||||||||||||||||||||||:||
Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLSSS 222


RESULT 7
AAY02340
ID   AAY02340 standard; Protein; 222 AA.
XX
AC   AAY02340;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Canine Interleukin-12 (IL-12) protein sequence.
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease.
XX
OS   Canis sp.
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   N-PSDB; AAX35616.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence represents canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence   222 AA;

  Query Match             97.4%;  Score 1099;  DB 20;  Length 222;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-103;
  Matches  217;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MCPARSLLLVATLVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
```

```
Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||||||||||||:||
Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLSSS 222


RESULT 8
AAW84372
ID   AAW84372 standard; Protein; 222 AA.
XX
AC   AAW84372;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03153.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   222 AA;

  Query Match             97.4%;  Score 1099;  DB 20;  Length 222;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-103;
  Matches  217;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  ||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 MCPARSLLLVATLVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||||||||||||:||
Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLSSS 222


RESULT 9
AAG66481
ID   AAG66481 standard; Protein; 222 AA.
XX
AC   AAG66481;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..25
FT                   /label= Signal_peptide
FT   Protein         26..222
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64379.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   222 AA;

  Query Match             97.4%;  Score 1099;  DB 22;  Length 222;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-103;
  Matches  217;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  ||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 MCPARSLLLVATLVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||||||||||||:||
Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLSSS 222


RESULT 10
AAW76175
ID   AAW76175 standard; Protein; 222 AA.
XX
AC   AAW76175;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 protein.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..25
FT                   /label= signal
FT   Protein         26..222
FT                   /label= FLAFp35
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   N-PSDB; AAV56628.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 8; Page 49-51; 94pp; Japanese.
XX
CC   This sequence represents a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence   222 AA;

  Query Match            92.7%;  Score 1046;  DB 19;  Length 222;
  Best Local Similarity  92.3%;  Pred. No. 4.5e-98;
  Matches  205;  Conservative    8;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              |||||||||||||||:|||||: ||:||| :||||:|||||||| ||||:|||||||||
Db          1 MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASGKAS 120
              ||| |||||||||||||||||||||||||||||||||||||||||| | |
Db         61 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASRKTS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| |||||||||||||:|||||||||||||||||||||||||||||| |||||
Db        121 FMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              || |||||||||||||||||||||||||:|||||||||
Db        181 PQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 222


RESULT 11
AAW74325
ID   AAW74325 standard; Protein; 197 AA.
XX
AC   AAW74325;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p35 subunit.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   N-PSDB; AAX18179.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 1; Page 28-29; 51pp; Japanese.
XX
CC   This sequence is the canine lymphocyte activation factor (CLAF) of .
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence   197 AA;

  Query Match            88.1%;  Score 994;  DB 20;  Length 197;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-93;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60

Qy         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120

Qy        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180

Qy        206 RIRAVTIDRMMSYLNSS 222
              |||||||||||||||||
Db        181 RIRAVTIDRMMSYLNSS 197


RESULT 12
AAE08606
ID   AAE08606 standard; Protein; 219 AA.
XX
AC   AAE08606;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 from clone R2-796.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Leader_peptide
FT   Protein         23..219
FT                   /note= "Mature modified p35"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   N-PSDB; AAD15213.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 124; Fig 11; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein.
XX
SQ   Sequence   219 AA;

  Query Match             85.8%;  Score 967.5;  DB 22;  Length 219;
  Best Local Similarity   86.9%;  Pred. No. 4.2e-90;
  Matches  193;  Conservative    8;  Mismatches   18;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              |||||||||||  |||   |||| |||:|| |:| ||:| ||:||||||||||| ||||||
Db          1 MCPPRGLLLVATLVL---LDHLSLARNLPVATPGPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| |||||||||||||||||||||||||  ||||| ||| | ||||||||| | |
Db         58 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| |||||||||||||:||| |||||||:|||||||||||||||||||||||| ||
Db        118 FMTTLCLSSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNMLTAIDELLQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||:|||||||||
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 219


RESULT 13
AAE08613
ID   AAE08613 standard; Protein; 219 AA.
XX
AC   AAE08613;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 from clone R1-4-87.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Leader_peptide
FT   Protein         23..219
FT                   /note= "Mature modified p35"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   N-PSDB; AAD15220.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 124; Fig 11; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein.
XX
SQ   Sequence   219 AA;

  Query Match             85.8%;  Score 967.5;  DB 22;  Length 219;
  Best Local Similarity   86.9%;  Pred. No. 4.2e-90;
  Matches  193;  Conservative    8;  Mismatches   18;  Indels    3;  Gaps    1;
```

```
Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||||||||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||| ||||||
Db          1 MCPPRGLLLVATLVL---LDHLSLARNLPVATPGPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| |||||||||||||||||||||||||||  ||||| ||| | |||||||| | |
Db         58 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| ||||||||||||:||| |||||||:||||||||||||||||||||||||| ||
Db        118 FMTTLCLSSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNMLTAIDELLQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              |||||||||||||||||||||||||||||||:|||||||||
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 219
```

RESULT 14
AAE08610
ID AAE08610 standard; Protein; 219 AA.
XX
AC AAE08610;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 from clone R2-555.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW human; p35; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= Leader_peptide
FT Protein 23..219
FT /note= "Mature modified p35"
XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32664.
XX
PR 02-DEC-1999; 99US-0169035.
PR 28-NOV-2000; 2000US-0169035.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR N-PSDB; AAD15217.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT p40 and p35 polypeptides), useful for treating various diseases e.g.
PT diabetic retinopathy and cancer -
XX
PS Claim 124; Fig 11; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein.
XX
SQ Sequence 219 AA;

```
  Query Match             85.3%;  Score 962.5;  DB 22;  Length 219;
  Best Local Similarity   86.5%;  Pred. No. 1.4e-89;
  Matches  192;  Conservative    8;  Mismatches   19;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||||||||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||| ||||||
Db          1 MCPPRGLLLVATLVL---LDHLSLARNLPVATPGPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| ||||||| |||||||||||||||||||  ||||| ||| | |||||||| | |
Db         58 TLEFYSCTSEETDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| ||||||||||||:||| |||||||:||||||||||||||||||||||||| ||
Db        118 FMTTLCLSSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNMLTAIDELLQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              |||||||||||||||||||||||||||||||:|||||||||
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 219
```

RESULT 15
AAE08609
ID AAE08609 standard; Protein; 219 AA.
XX
AC AAE08609;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 from clone R2-571.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW human; p35; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= Leader_peptide
FT Protein 23..219
FT /note= "Mature modified p35"
XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32664.
XX
PR 02-DEC-1999; 99US-0169035.
PR 28-NOV-2000; 2000US-0169035.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR N-PSDB; AAD15216.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT p40 and p35 polypeptides), useful for treating various diseases e.g.
PT diabetic retinopathy and cancer -
XX
PS Claim 124; Fig 11; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and

CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein.
XX
SQ Sequence 219 AA;

Query Match 85.0%; Score 958.5; DB 22; Length 219;
Best Local Similarity 86.5%; Pred. No. 3.5e-89;
Matches 192; Conservative 8; Mismatches 19; Indels 3; Gaps 1;

```
Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   |||| : ||:|| |:| ||:| ||:||||||||||| ||||||
Db          1 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| ||||||||||||||||||||||||||||  |||||||| |||||||||||| | |
Db         58 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRGISLITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| ||| |||||||||||:||| |||||||:|||||||||||||||||||||||||| ||
Db        118 FMTTLCLGSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNMLTAIDELLQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||:|||||||||
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 219
```

Search completed: July 15, 2003, 11:02:51
Job time : 24.3163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:49 ; Search time 9.73035 Seconds
(without alignments)
2193.328 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	940.5	83.4	253	2	B38957	interleukin 12A pr
2	591.5	52.4	215	2	I56135	interleukin 12 p35
3	97.5	8.6	816	2	D84601	hypothetical prote
4	96.5	8.6	2504	1	A57788	enoyl-[acyl-carrie
5	93	8.2	1583	2	F97846	hypothetical prote
6	90	8.0	615	2	T20187	hypothetical prote
7	89.5	7.9	383	2	F71550	probable endonucle
8	87.5	7.8	1957	2	T38077	hypothetical coile
9	86.5	7.7	1134	2	S53955	hypothetical prote
10	86	7.6	446	2	C85343	hypothetical prote
11	86	7.6	1286	2	T16507	hypothetical prote
12	85.5	7.6	586	2	F64186	ABC-type transport
13	85.5	7.6	849	2	C97303	hypothetical prote
14	85	7.5	1476	2	A41185	alpha-2 macroglobu
15	84.5	7.5	310	2	T33611	hypothetical prote
16	84.5	7.5	857	2	F81396	ATP-dependent CLP
17	83.5	7.4	363	2	T22594	hypothetical prote
18	83.5	7.4	505	2	T01667	gag polyprotein -
19	83.5	7.4	1040	2	AH1926	hypothetical prote
20	83	7.4	1061	2	JC7116	Xsal-3 protein - A
21	82.5	7.3	271	2	AB1292	amino acid ABC tra
22	82.5	7.3	523	2	D86492	hypothetical prote
23	82.5	7.3	523	2	D72130	hypothetical prote
24	82.5	7.3	607	2	D64603	hypothetical prote
25	82.5	7.3	640	2	C72351	hypothetical prote
26	82.5	7.3	2509	2	G01880	fatty-acid synthas
27	82	7.3	595	2	JC6550	sex-determining re
28	82	7.3	629	2	E64046	mismatch repair pr
29	82	7.3	649	2	T32668	hypothetical prote
30	82	7.3	870	2	A96637	hypothetical prote
31	81	7.2	237	2	S70797	vsaE1 protein - My
32	81	7.2	309	2	S70793	vsaE2 protein - My
33	81	7.2	314	2	F90577	lipoprotein vsaE [
34	81	7.2	357	2	S29275	hypothetical prote
35	80.5	7.1	214	2	JC5043	granulocyte colony
36	80.5	7.1	808	2	C72858	AcOrf-66 protein -
37	80.5	7.1	821	2	T24728	hypothetical prote
38	80.5	7.1	1349	2	AI1476	cell surface prote
39	80	7.1	290	2	T21859	hypothetical prote
40	80	7.1	307	2	AF2402	hypothetical prote
41	80	7.1	315	2	T37674	conserved hypothet
42	80	7.1	465	2	A84548	probable protein k
43	80	7.1	1094	2	S22573	DNA-directed DNA p
44	80	7.1	1939	2	T18372	repeat organellar
45	79.5	7.0	281	1	I40679	beta-hydroxybutyry

ALIGNMENTS

RESULT 1
B38957
interleukin 12A precursor [validated] - human
N;Alternate names: cytotoxic lymphocyte maturation factor 35K chain; natural killer c
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 01-Dec-2000
C;Accession: B38957; A39359; A36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric
A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: B38957
A;Molecule type: mRNA
A;Residues: 1-253 <WOL>
A;Cross-references: GB:M65290
A;Note: it is uncertain whether Met-1 or Met-35 is the initiator
R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nab
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactiv
A;Reference number: A39359; MUID:91239523; PMID:1674604
A;Accession: A39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 35-246,'T',248-253 <GUB>
A;Cross-references: GB:M65271; GB:M38443; NID:g180623; PIDN:AAA35694.1; PID:g180624
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lympho
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: A36055
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'X',58-70,'X',72-82 <STE>
C;Genetics:
A;Gene: GDB:IL12A; NKSF1
A;Cross-references: GDB:127869; OMIM:161560
A;Map position: 3p12-3q13.2
C;Keywords: cytokine; glycoprotein; heterodimer
F;57-253/Product: interleukin 12A #status predicted <MAT>
F;127,141,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.4%; Score 940.5; DB 2; Length 253;
Best Local Similarity 84.2%; Pred. No. 1.1e-75;
Matches 187; Conservative 9; Mismatches 23; Indels 3; Gaps 1;

```
Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||||| ||||||
Db         35 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 91

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | ||||||||||||||||||||||||||||| ||||| ||| | |||||||| | |
```

```
Db          92 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 151

Qy         121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               ||  |||||||||||||:||| ||||||||||||||||||  ||||:||||||| ||
Db         152 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 211

Qy         181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               ||||||||||||||||||||||||||||||||:|||||:|
Db         212 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 253


RESULT 2
I56135
interleukin 12 p35 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I56135
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.;
J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I56135
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: GB:M86672; NID:g198336; PIDN:AAA39292.1; PID:g198337

  Query Match             52.4%;  Score 591.5;  DB 2;  Length 215;
  Best Local Similarity   54.5%;  Pred. No. 6.5e-45;
  Matches  121;  Conservative   36;  Mismatches   58;  Indels    7;  Gaps    2;

Qy           1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
               ||  | || :  | |   |:||: || :| : |:    :||: |:|||:   : :: ||:
Db           1 MCQSRYLLFLATLAL---LNHLSLARVIPVSGPA----RCLSQSRNLLKTTDDMVKTARE 53

Qy          61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
               |: ||||:|:|||||||:|:|||:: ||||||  ||||||:|| |  | ||||   | |
Db          54 KLKHYSCTAEDIDHEDITRDQTSTLKTCLPLELHKNESCLATRETSSTTRGSCLPPQKTS 113

Qy         121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               |  ||| |||||||||| ||:|:|| |     :|| ||: || |||||:|:|| |  |:
Db         114 LMMTLCLGSIYEDLKMYQTEFQAINAALQNHNHQQIILDKGMLVAIDELMQSLNHNGETL 173

Qy         181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               ||  : | | |: |:|||||||||  | |||:|:| ||:|:
Db         174 RQKPPVGEADPYRVKMKLCILLHAFSTRVVTINRVMGYLSSA 215


RESULT 3
D84601
hypothetical protein At2g21450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D84601
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84601
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-816 <STO>
A;Cross-references: GB:AE002093; NID:g4567276; PIDN:AAD23689.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g21450
A;Map position: 2

  Query Match              8.6%;  Score 97.5;  DB 2;  Length 816;
  Best Local Similarity   23.2%;  Pred. No. 1.7;
  Matches   52;  Conservative   34;  Mismatches   79;  Indels   59;  Gaps    9;

Qy          45 QNLLRAVSNTLQKARQ-------TLELYS--CTSEEIDHEDITKDKTSTVEACL--PLEL 93
               || :  | | |   |         | |: |   :  ||          :|::|      :||
Db         442 QNNVEEVFNILDLVRPKFLKRPGTREIVSRIMSKAEIPRGKQVNQSSSSIEGTFFAAVEL 501

Qy          94 TMNESCLASREISLI--------------TNGSCLASGKASFMTVLCLSSIYED----- 133
               |:  |   | : |||               : | |  | : |  :| |||| |
Db         502 TLQRSTNFSAKASLIKDLREMTRNILHYHKADFSGLLPGLSEFTVMLNLSSIQRDEVKGL 561

Qy         134 LKMYQMEFKAMNAKLLMDPKRQIFLDQN------------MLTAIDELLQALNFNSVTV 180
                ||   :  :: | | : || : ||::|             :  :|::|: :|     |
Db         562 RKMELFKQISLGAALYIHPKLKSFLEENPSNGEKGFSDNNTTVMKLDKMLKKINVRD-GV 620

Qy         181 PQKSSLEEPDFYKTKIKLC-------ILLHAFRIRAVTIDRMMS 217
               |       |:   : ||       ::   : :   |::|:||
Db         621 KMK-------FFLNLLALCESTGEKLLVFSQYIVPIKTLERLMS 657


RESULT 4
A57788
enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific) (EC 1.3.1.10) (version 1)
N;Contains: 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.61); 3-ox
oyl-[acyl-carrier-protein] reductase (NADPH, B-specific) (EC 1.3.1.10); oleoyl-[acyl-
protein] S-malonyltransferase (EC 2.3.1.39)
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 10-Jul-1998 #text_change 03-Jun-2002
C;Accession: A57788; B57788
R;Jayakumar, A.; Tai, M.H.; Huang, W.Y.; al-Feel, W.; Hsu, M.; Abu-Elheiga, L.; Chira
Proc. Natl. Acad. Sci. U.S.A. 92, 8695-8699, 1995
A;Title: Human fatty acid synthase: properties and molecular cloning.
A;Reference number: A57788; MUID:96004605; PMID:7567999
A;Accession: A57788
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2504 <JAY1>
A;Cross-references: EMBL:U26644; NID:g1049052; PIDN:AAC50259.1; PID:g1049053
A;Accession: B57788
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1297,'TPTQDASSLSSLSYQQVA',1316-2504 <JAY2>
C;Genetics:
A;Gene: GDB:FASN
A;Cross-references: GDB:342064; OMIM:600212
A;Map position: 17q25-17q25
C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I h
ydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein]
C;Keywords: acyltransferase; carbon-oxygen lyase; carrier protein; coenzyme A; fatty
r hydrolase
F;22-403/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F;492-773/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1315-1333/Region: catalytic (of 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydrata
F;1545-1849/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;1664-1694/Region: beta-alpha-beta NADP nucleotide-binding fold
F;1879-2061/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;2116-2186/Domain: acyl carrier protein homology <ACP>
F;2212-2504/Domain: oleoyl-[acyl-carrier-protein] hydrolase #status predicted <ENZ7>
F;2228-2480/Domain: oleoyl-[acyl-carrier-protein] hydrolase homology <ACPH>
F;161/Active site: Cys (of 3-oxoacyl-[acyl-carrier-protein] synthase) #status predict
F;580/Active site: Ser (covalent substrate-binding) (of [acyl-carrier-protein] S-malo
F;1696,1699/Active site: Ser, Lys (of enoyl-[acyl-carrier-protein] reductase) #status
F;1921/Active site: Lys (of 3-oxoacyl-[acyl-carrier-protein] reductase) #status predi
F;2151/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
F;2302/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status predicte

  Query Match              8.6%;  Score 96.5;  DB 1;  Length 2504;
  Best Local Similarity   22.7%;  Pred. No. 8.6;
  Matches   60;  Conservative   34;  Mismatches   87;  Indels   83;  Gaps   13;

Qy           4 PRGLLLVTILVLLSHLDHLTW----ARSLP--TASPSPGIFQCLNHSQN---------- 46
               |||  |:: |:   |   | |    |   |  : |||  |: |   |::
Db         822 PRGTPLISPLIKWDH--SLAWDAPAAEDFPNGSGSPSATIYTCTPSSESPDRYLVDHTID 879

Qy          47 ---------LLRAVSNTLQKARQTLELYSCTSEE-IDHEDITKDKTSTVEACLPLELTMN 96
                        |  |  || :|   ||      |: : |:     || ||     ||: :
```

```
Db        880 GRVLFPATGYLSIVWKTLARAWAGLEQLPVVFEDVVQHQATILPKTGTVS----LEVRLL 935

Qy         97 ESCLASREISLITNGSCLASGKA----------------------SFMTVLCLSSIYEDL 134
              |   |:    :  ||: : |||                       |  : :|::|
Db        936 E---ATGAFEVSENGNLVVSGKVYQWDDPDPRLFDHPESPHPNSPRSPLFLAQAEVYKEL 992

Qy        135 KM----YQMEFKA-MNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEP 189
              ::    |   |:  : | |  |  | :: | | :: :| :||     |:    |  |  |
Db        993 RLRGYDYGPHFQGILEASLEGDSGRLLWKD-NWVSFMDTMLQM----SILGSAKHGLYLP 1047

Qy        190 DFYKTKIKLCILLHAFRIRAVTID 213
                          |: |: ||
Db       1048 T---------------RVTAIHID 1056


RESULT 5
F97846
hypothetical protein RC1174 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: F97846
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: F97846
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1583 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL03712.1; PID:g15620302; GSPDB:GN00173
C;Genetics:
A;Gene: RC1174

  Query Match             8.2%;  Score 93;  DB 2;  Length 1583;
  Best Local Similarity   22.6%;  Pred. No. 9.7;
  Matches   47;  Conservative   40;  Mismatches   71;  Indels   50;  Gaps    9;

Qy         34 SPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLEL 93
              | |:  | :|  |:  |:|: :   : |||        :   :  | |  ||     ||
Db       1140 SAGV-DCSDHEVNIKIALSSAITSGKITLE---------ERNKLLNDMTKQVE-----EL 1184

Qy         94 TMNESCLASREISLITNGSCLASGKASFMTVLCLS---SIYEDLKMYQME---------- 140
                : ::   :  |:::     |       ||  ||    | |: |: : |
Db       1185 VLIDNYKQTEAITIMQLSPTL--------TVNILSQFIDILEEEKVLERENEFLPSAEEL 1236

Qy        141 -FKAMNAKLLMDPKRQIFLDQNMLTAIDELLQAL-----NFNSVTVPQKSSLEEPDFYKT 194
               :||: ::|  |:  | |  :  :|  ||: :       |::  :        |:  :
Db       1237 NSRAMSGEVLTRPELCILLSYSKRSAYHELINSTFSHDKYFDAYLIDY-----FPEMMQK 1291

Qy        195 KIKLCILLHAFR---IRAVTIDRMMSYL 219
              | :  || |  :    |: |||:::|: |
Db       1292 KFRNEILSHPLKHEIIKTVTINKIMNQL 1319


RESULT 6
T20187
hypothetical protein C53D6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20187
R;Gardner, A.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19235
A;Accession: T20187
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-615 <WIL>
A;Cross-references: EMBL:Z70270; PIDN:CAA94225.1; GSPDB:GN00022; CESP:C53D6.6
A;Experimental source: clone C53D6
C;Genetics:
A;Gene: CESP:C53D6.6
A;Map position: 4
A;Introns: 44/1; 387/3; 447/3; 528/3

  Query Match             8.0%;  Score 90;  DB 2;  Length 615;
  Best Local Similarity   25.1%;  Pred. No. 5.3;
  Matches   43;  Conservative   30;  Mismatches   62;  Indels   36;  Gaps    9;

Qy         51 VSNTLQKARQTLE--LYSCTSEEIDHEDIT-----KDKTSTVEACLPLELTMNESCLASR 103
              ||| |: : | ||  :| ||    :    |:         |  :| |  :   :||| :
Db        251 VSN-LKLSAQLLEFDIYDCTWNSLSLASISGINTIPGGTELIEKCKKIVQKINESAVYET 309

Qy        104 ----EISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLD 159
                  |   | :   : ||| :::||:   |::|       : | :   ||:    : |
Db        310 SLIGEYMTIDSADLVKSGKLNWITVV---SMFEQF----TKLKGLLDTFLMNDMEGLMLY 362

Qy        160 QNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAV 210
              |      :: :|: |:      | |:::   || |         | ||| |:
Db        363 QQDYDLMEIILRTLS------PLKTAV---DFGKQ--------HTFRISAI 396


RESULT 7
F71550
probable endonuclease CT154 [similarity] - Chlamydia trachomatis (serotype D, strain
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 04-Feb-2000
C;Accession: F71550
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: F71550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-383 <ARN>
A;Cross-references: GB:AE001289; GB:AE001273; NID:g3328550; PIDN:AAC67745.1; PID:g332
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: CT154

  Query Match             7.9%;  Score 89.5;  DB 2;  Length 383;
  Best Local Similarity   26.7%;  Pred. No. 3.2;
  Matches   36;  Conservative   26;  Mismatches   54;  Indels   19;  Gaps    5;

Qy         21 HLTWARS--LPTASPSPG----------IFQCLNHSQ--NLLRAVSNTLQKARQ--TLEL 64
              |:| ::|  ||     |           ||  ::  |  | || : :|:::|::   : :
Db         30 HVTRSQSSALPQLQERPVPHPLAERELIIFHSVHQQQNNNPLRMICDTIRQAQRGIFMRI 89

Qy         65 YSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGK---ASF 121
              |: :|::|    |       ||       ::  :|  || :  :|||  |    |   | |
Db         90 YTISSDDIIQSLIQTSHHVPVEVKYHCGESLPVACQNSRVVLRLTNGRTLQHKKTMLADF 149

Qy        122 MTVLCLSSIYEDLKM 136
               ||:  |: | || :
Db        150 QTVVTGSANYTDLSL 164


RESULT 8
T38077
hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38077
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z21767
A;Accession: T38077
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1957 <CON>
A;Cross-references: EMBL:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
A;Experimental source: strain 972h-; cosmid c1F3
C;Genetics:
A;Gene: SPDB:SPAC1F3.06c
A;Map position: 1
```

```
  Query Match             7.8%;  Score 87.5;  DB 2;  Length 1957;
  Best Local Similarity   20.7%;  Pred. No. 39;
  Matches   51;  Conservative   51;  Mismatches   87;  Indels   57;  Gaps    9;

Qy          8 LLVTILVLLSHLDHLTWARSLPTASPSPGIFQCL-NHSQNLLRAVSNTLQKARQTLELYS 66
              |:  |  : | ||  ::   | :|    |  | | : | :|:  : : ||:|:: :::
Db       1458 LMEKIESINSSLDDKSF--ELASAVEKLGALQKLHSESLSLMENIKSQLQEAKEKIQVDE 1515

Qy         67 CTSEEIDHE----------------DITKDKTSTVEA---CLPLELTMNESCLASREISL 107
               | :|:|||                | :| :  :|     |  | : :    :|  :
Db       1516 STIQELDHEITASKNNYEGKLNDKDSIIRDLSENIEQLNNLLAEEKSAVKRLSTEKESEI 1575

Qy        108 ITNGSCLAS------------GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQ 155
              :   | ||            |::     | |:|  |:|:: : |  ::  ::| | : |
Db       1576 LQFNSRLADLEYHKSQVESELGRSK----LKLASTTEELQLAENERLSLTTRML-DLQNQ 1630

Qy        156 IFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRM 215
              :    |:  :: | |: |           |||:         :  |    :|:: |:: :
Db       1631 VKDLSNIKDSLSEDLRTLR----------SLED--------SVASLQKECKIKSNTVESL 1672

Qy        216 MSYLNS 221
                | |
Db       1673 QDVLTS 1678


RESULT 9
S53955
hypothetical protein YML117w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8339.02
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S53955
R;Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S53954
A;Accession: S53955
A;Molecule type: DNA
A;Residues: 1-1134 <SKE>
A;Cross-references: EMBL:Z49210; NID:g798881; PIDN:CAA89101.1; PID:g798883; GSPDB:GN0001
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YML117w
A;Cross-references: SGD:S0004585
A;Map position: 13L

  Query Match             7.7%;  Score 86.5;  DB 2;  Length 1134;
  Best Local Similarity   24.8%;  Pred. No. 24;
  Matches   50;  Conservative   27;  Mismatches   54;  Indels   71;  Gaps   12;

Qy         40 CLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDH----EDITKD--KTSTVEACLPLE- 92
              |:|:       |  |    | :|  |      | :||      | |:  |::|:|:   :|
Db        198 CINYK------VLPTGDDAYRTRSL---LIENVDHSIDLHSIVKNFVKSNTLESAYLIEG 248

Qy         93 ---------LTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFK- 142
                      | | | |    || :| | ||              : | ::     |||
Db        249 GKSDDSKDVETKNLSIL----ISFLTKGDCL-------------NFYNNILQRLSEFKT 290

Qy        143 -----AMNAK---LLMDPK-RQIFLDQNMLTAIDE----------LLQALNFN------- 176
                  |:| |   |  |||    |::   ||   |           :  :|: |
Db        291 FLKSEALNLKFVCLNYDPKCLPTFIESEALTENAEEADITNGSTMISASLHHNIANKDAT 350

Qy        177 -SVTVPQKSSLEEPDFYKTKIK 197
               |: :  || :|: | :| |::
Db        351 RSIIIEFKSPVEKSDLFKKKLQ 372


RESULT 10
C85343
hypothetical protein AT4g29420 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: C85343
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85343
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-446 <STO>
A;Cross-references: GB:NC_001268; NID:g7269841; PIDN:CAB79700.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4g29420
A;Map position: 4

  Query Match             7.6%;  Score 86;  DB 2;  Length 446;
  Best Local Similarity   22.6%;  Pred. No. 8;
  Matches   45;  Conservative   39;  Mismatches   71;  Indels   44;  Gaps   10;

Qy         23 TW-----ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDI 77
              ||     :||:   :|   ||: |  : : :|::|  : || : :       |  | :|:
Db         47 TWSRYLKSRSIVVVTPFKTIFRSLIENSSKIRSISVGVDKALKGMSFDDFNEE--DSKDL 104

Qy         78 TKDKTSTVEACLP-----LE-LTMN----ESCLASREISLITNGSC----LASGKASFMT 123
                        |:  ||     || |:::    :||    :|  : : :|        | ::::
Db        105 YLTDVEFVKEWLPRVREDLENLSISDFWIQSCWRKSDILALISSNCSKLVKLEVKNAWLS 164

Qy        124 VLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDE---LLQALNFNSVTV 180
              |: |: :  :|:   :||              | ||   |  :::    || ||   |
Db        165 VVGLTEM-PNLRYLTLEF-------------IRLDDENLEKVNDCFPFLQELNLIGV-- 207

Qy        181 PQKSSLEEPDFYKTKIKLC 199
                  |:||  :   :| |
Db        208 ---GGLKEPRIHFLHLKSC 223


RESULT 11
T16507
hypothetical protein F59A6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16507
R;Nhan, M.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F59A6.
A;Reference number: Z18526
A;Accession: T16507
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1286 <NHA>
A;Cross-references: EMBL:U41994; NID:g1123047; PID:g1123050; PIDN:AAA83454.1; CESP:F5
C;Genetics:
A;Gene: CESP:F59A6.5
A;Introns: 35/3; 335/3; 685/3; 973/3; 1097/3

  Query Match             7.6%;  Score 86;  DB 2;  Length 1286;
  Best Local Similarity   23.8%;  Pred. No. 31;
  Matches   41;  Conservative   28;  Mismatches   71;  Indels   32;  Gaps    6;

Qy         41 LNHSQNLLRAVSN---TLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNE 97
              | | |: :| : |   ||:  :|||:      | |      | :| |      || : :
Db        109 LKHHQSQIRILQNKCSTLEMEKQTLQ------ETIQRAQDDKKETET-----ELESSRSR 157

Qy         98 SCLASREISLITN-----------GSCLASGKASFMTVLC-----LSSIYEDLKMYQME 140
                :  :|:|   |             | | :  ::| |        :: | |: |: :
Db        158 LHVLEKELSAKANDIFMVTKDLHDKNEELTSFRMEYVTKLSEANREKKALEEKLEKYKND 217

Qy        141 FKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFY 192
                |  : | |   | |:   ||:|: : :|     | :      | : | | |
Db        218 MKENDRKSLELNKEQV-TTQNVLSEVRQLSAHFEFLTPVRKNASKIRELDEY 268


RESULT 12
F64186
ABC-type transport protein cydD - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
```

```
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 02-Feb-2001
C;Accession: F64186
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64186
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-586 <TIGR>
A;Cross-references: GB:U32795; GB:L42023; NID:g1574708; PIDN:AAC22812.1; PID:g1574714; T
C;Genetics:
A;Gene: cydD
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop; transmembrane protein; transport protein
F;23-39/Domain: transmembrane #status predicted <TM1>
F;66-82/Domain: transmembrane #status predicted <TM2>
F;145-161/Domain: transmembrane #status predicted <TM3>
F;167-183/Domain: transmembrane #status predicted <TM4>
F;252-268/Domain: transmembrane #status predicted <TM5>
F;285-301/Domain: transmembrane #status predicted <TM6>
F;366-557/Domain: ATP-binding cassette homology <ABC>
F;383-390/Region: nucleotide-binding motif A (P-loop)

  Query Match             7.6%;  Score 85.5;  DB 2;  Length 586;
  Best Local Similarity   21.8%;  Pred. No. 12;
  Matches   51;  Conservative   35;  Mismatches   73;  Indels   75;  Gaps   10;

Qy          3 PPRGLLLVTILVLLSHLDHLTWARSLPTASPSP---------GIFQCLNHSQN---LLRA 50
              | : |  :  :|:   :  | ||  |     :|         ||    |  :|   | |
Db        142 PQQSLSAIVPVVIFIAVFPLNWAAGLILMITAPLVPLFMIIVGIAAADNSQKNMDTLSRL 201

Qy         51 VSNTLQKAR--QTLELYSCTSEEIDH-EDITKDKTSTVEACLPLELTMNESCLASREISL 107
               :  | : |  :|| |:: |||: :| |: |:|   |    | |      : |:|  :
Db        202 SAQFLDRLRGLETLRLFNRTSEQTEHIENATEDFRETTMDVLKL------AFLSSAVLEF 255

Qy        108 ITNGSCLASGKASFMTVLCLSSIYEDLK-MYQMEFKAMNAKLLM--------------DP 152
              |: |           : | ::|     : |:||   || | :               |
Db        256 FTSIS------------IALMAVYFGFSYLGQIEFGTYNAPLTLFTGFFCLILAPEFYQP 303

Qy        153 KRQI-------------------FLDQNMLTAIDELLQALNFNSVTVPQKSSLE 187
              | :                   ||: : ||        :: |  |:  :|::|
Db        304 LRDLGTYYHDRAAGIGAADAIVDFLESDYLT--------VHQNEKTISLESAVE 349


RESULT 13
C97303
hypothetical protein CAC3280 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C97303
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97303
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-849 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81214.1; PID:g15026357; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3280

  Query Match             7.6%;  Score 85.5;  DB 2;  Length 849;
  Best Local Similarity   24.4%;  Pred. No. 20;
  Matches   51;  Conservative   33;  Mismatches   86;  Indels   39;  Gaps    9;

Qy         16 LSHLDHLTWARSLPTASPSPGIFQCLNH--SQNLLRAVSNTLQ--------KARQTLELY 65
              :| | :||    |  ::       ||:    |:|   || :         |  ||| |
Db        635 ISALSNLTNLNQLDLSTNQISNISSLNNLIGLNILNLNSNKINDISSLTNLKQLQTLSLN 694

Qy         66 SCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS----REISL----ITNGSCLAS- 116
              | | ::|   |: |: |      |      : | ||:    : |||    ||| ||| :
Db        695 SNTIQDI---DVLKNFTVLNVLGLSNNKITDISTLANLNSLKNISLSNNQITNISCLCNL 751

Qy        117 GKASFM--------TVLCLSSIYEDLKMY--QMEFKAMNAKLLMDPKRQIFLDQNMLTAI 166
                | ::         :  |: :     :|    :   : |   :|    ::|  | :| :
Db        752 TNAQYLHLENNQINDISALNKLKNLAYLYLNNNQITDITALGFLDKLNTLYLSYNKITKV 811

Qy        167 DELLQALNF-------NSVTVPQKSSLEE 188
              | |    |        |::|   ::||:|
Db        812 DSLKNLTNLKILILAENNITSTDQTSLKE 840


RESULT 14
A41185
alpha-2 macroglobulin MUG1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 12-Apr-1995
C;Accession: A41185
R;Overbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
J. Biol. Chem. 266, 16903-16910, 1991
A;Title: Molecular characterization of the murinoglobulins.
A;Reference number: A41185; MUID:91358495; PMID:1840592
A;Accession: A41185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1476 <OVE>
A;Cross-references: GB:M65736
C;Superfamily: alpha-2-macroglobulin

  Query Match             7.5%;  Score 85;  DB 2;  Length 1476;
  Best Local Similarity   24.2%;  Pred. No. 45;
  Matches   38;  Conservative   30;  Mismatches   47;  Indels   42;  Gaps    8;

Qy         99 CLASREISLITNGSCLASGKASFMTVLCLSSIYED------LKMYQM-EFKAMNAKLLMD 151
              || |  :: : : | | :| : :| ||  | :| :      | :||: |   : | |:
Db         10 CLFSVLLAFLHSAS-LLNGDSKYM-VLVPSQLYTETPEKICLHLYQLNETVTVTASLVSQ 67

Qy        152 PKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIK---------LCILL 202
                |:   |: :|    :| | ::|    :|: || :| ||    ||          :|:
Db         68 SGRKNLFDELVLD--KDLFQCVSF---IIPRLSSSDEEDFLYVDIKGPTHEFSKRKAVLV 122

Qy        203 -------------------HAFRIRAVTIDRMMSYLN 220
                                : : | |::|:|:  ||
Db        123 KNKESVVFVQTDKPVYKPGQSVKFRVVSMDKMLRPLN 159


RESULT 15
T33611
hypothetical protein F54D10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33611
R;Sammons, L.; Wohldmann, P.; Clarke, K.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid F54D10.
A;Reference number: Z21377
A;Accession: T33611
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-310 <SAM>
A;Cross-references: EMBL:AF099917; PIDN:AAC68781.1; GSPDB:GN00020; CESP:F54D10.3
A;Experimental source: strain Bristol N2; clone F54D10
C;Genetics:
A;Gene: CESP:F54D10.3
A;Map position: 2
A;Introns: 162/2; 234/3

  Query Match             7.5%;  Score 84.5;  DB 2;  Length 310;
  Best Local Similarity   22.0%;  Pred. No. 6.8;
```

```
  Matches   40;  Conservative   41;  Mismatches   54;  Indels   47;  Gaps   10;

Qy          46 NLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREI 105
               ||:: |   : : ::  :|:: ::::|| |     :  ||     :||      | |  :
Db          22 NLIKKVFLNILEPKE--DLWN-SNQKIDRE-----RWETV----GIELFQRTGILVS--V 67

Qy         106 SLITNG------------SCLASGKASFMTVLCLS--SIYEDLKMYQMEF--------- 141
                 : :|             :|: || :   | | |    :::||: |  :
Db          68 DQMRSGFRSIKSNLGQRLHNCVQSGMSRIQTELELQKWELFQDLRFYYDKLYKYRQLRAE 127

Qy         142 ----KAMNAKLLMDPKRQIFLDQ-NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKI 196
                   :| |:: :     | | :: :|:: ::|   |: : |  :|| ||   |    ||:
Db         128 RTGNEARNSEPVSGEDMQSFFEEPDMMSLVEENDSAMKYLSSLIPQVSSTSTP----TKV 183

Qy         197 KL 198
               ||
Db         184 KL 185

Search completed: July 15, 2003, 11:08:40
Job time : 12.7303 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:28 ; Search time 4.86517 Seconds
(without alignments)
1892.583 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1107	98.1	222	1	I12A_CANFA	Q28267 canis famil
2	1043	92.5	222	1	I12A_FELCA	O02743 felis silve
3	967	85.7	222	1	I12A_HORSE	Q9xsq6 equus cabal
4	960	85.1	222	1	I12A_PIG	Q29053 sus scrofa
5	940.5	83.4	219	1	I12A_HUMAN	P29459 homo sapien
6	911.5	80.8	221	1	I12A_CEREL	Q28233 cervus elap
7	910.5	80.7	221	1	I12A_SHEEP	Q9tu27 ovis aries
8	908.5	80.5	221	1	I12A_BOVIN	P54349 bos taurus
9	893.5	79.2	221	1	I12A_CAPHI	O02814 capra hircu
10	888.5	78.8	219	1	I12A_MACMU	P48091 macaca mula
11	883.5	78.3	219	1	I12A_CERTO	P46661 cercocebus
12	636.5	56.4	223	1	I12A_MARMO	Q61728 marmota mon
13	591.5	52.4	215	1	I12A_MOUSE	P43431 mus musculu
14	96.5	8.6	2504	1	FAS_HUMAN	P49327 homo sapien
15	87.5	7.8	1957	1	YD86_SCHPO	Q10411 schizosacch
16	86.5	7.7	1134	1	YML7_YEAST	Q03735 saccharomyc
17	86	7.6	583	1	ESR1_OREAU	P50240 oreochromis
18	85.5	7.6	579	1	ESR1_SPAAU	Q9pvz9 sparus aura
19	85.5	7.6	586	1	CYDD_HAEIN	P45082 haemophilus
20	85	7.5	1476	1	A2M1_MOUSE	P28665 mus musculu
21	84.5	7.5	3210	1	CENF_HUMAN	P49454 homo sapien
22	84	7.4	734	1	G13B_DICDI	P34116 dictyosteli
23	84	7.4	1243	1	DPOA_ORYSA	O48653 oryza sativ
24	83.5	7.4	504	1	GAG_HV1MA	P04594 human immun
25	83.5	7.4	585	1	ESR1_ORENI	Q9yh33 oreochromis
26	82	7.3	357	1	YPH2_CHRVI	P45372 chromatium
27	82	7.3	629	1	MUTL_HAEIN	P44494 haemophilus
28	82	7.3	984	1	SX13_MOUSE	Q04891 mus musculu
29	81.5	7.2	581	1	ESR1_PAGMA	O42132 pagrus majo
30	80.5	7.1	355	1	GBAC_CAEEL	Q19572 caenorhabdi
31	80.5	7.1	808	1	Y066_NPVAC	P41467 autographa
32	80.5	7.1	821	1	LIN5_CAEEL	P45970 caenorhabdi
33	80	7.1	1018	1	ST31_MOUSE	Q99mw1 mus musculu
34	80	7.1	1094	1	DPOD_PLAFK	P30315 plasmodium
35	79.5	7.0	281	1	HBD_CLODI	P45364 clostridium
36	79.5	7.0	1548	1	SMCY_MOUSE	Q62240 mus musculu
37	79	7.0	571	1	SYQ_BUCAI	P57490 buchnera ap
38	79	7.0	2505	1	FAS_RAT	P12785 rattus norv
39	78	6.9	448	1	FDFT_CANAL	P78589 candida alb
40	78	6.9	1351	1	RPOM_YEAST	P13433 saccharomyc
41	77.5	6.9	358	1	YKT5_CAEEL	P34316 caenorhabdi
42	77	6.8	381	1	PRLP_BOVIN	Q9gkn8 bos taurus
43	77	6.8	1629	1	RRPO_SHMV	P89202 sunn-hemp m
44	76.5	6.8	189	1	INAB_BOVIN	P05008 bos taurus
45	76.5	6.8	501	1	GAG_HV1A2	P03349 human immun

ALIGNMENTS

RESULT 1
I12A_CANFA
ID I12A_CANFA STANDARD; PRT; 222 AA.
AC Q28267;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE maturation factor 35 kDa subunit) (CLMF p35).
GN IL12A.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98280561; PubMed=9617567;
RA Buettner M., Belke-Louis G.F., Rziha H.J., McInnes C., Kaaden O.R.;
RT "Detection, cDNA cloning and sequencing of canine interleukin 12.";
RL Cytokine 10:241-248(1998).
CC -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC BY RESTING PBMC (BY SIMILARITY).
CC -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC --
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CC --
DR EMBL; U49085; AAA92058.1; -.
DR InterPro; IPR004281; IL12.
DR Pfam; PF03039; IL12; 1.
KW Cytokine; Growth factor; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 222 INTERLEUKIN-12 ALPHA CHAIN.
FT DISULFID 99 99 INTERCHAIN (PROBABLE).
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 222 AA; 24992 MW; 48C7E53ECFD6ACE5 CRC64;

Query Match 98.1%; Score 1107; DB 1; Length 222;
Best Local Similarity 98.2%; Pred. No. 7e-89;
Matches 218; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

```
Qy          61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
               ||:  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy         121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy         181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               |||||||||||||||||||||||||||||||||||||||||||
Db         181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222


RESULT 2
I12A_FELCA
ID   I12A_FELCA     STANDARD;      PRT;   222 AA.
AC   O02743; O46672;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97246745; PubMed=9089110;
RA   Schijns V.E.C.J., Wierda C.M.H., Vahlenkamp T.W., Horzinek M.C.;
RT   "Molecular cloning of cat interleukin-12.";
RL   Immunogenetics 45:462-463(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98182592; PubMed=9522125;
RA   Fehr D., Dean G.A., Huder J., Fan Z., Huettner S., Higgins J.W.,
RA   Pedersen N.C., Lutz H.;
RT   "Nucleotide and predicted peptide sequence of feline interleukin-12
RT   (IL-12).";
RL   DNA Seq. 8:77-82(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; Y07761; CAA69067.1; -.
DR   EMBL; U83185; AAB93836.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD    42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   183    183       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    66     66       S -> P (IN REF. 2).
FT   CONFLICT   221    221       A -> S (IN REF. 2).
SQ   SEQUENCE   222 AA;  25076 MW;  223CF8FE0D30BF17 CRC64;

  Query Match             92.5%;  Score 1043;  DB 1;  Length 222;
  Best Local Similarity   91.9%;  Pred. No. 2.4e-83;
  Matches  204;  Conservative    9;  Mismatches    9;  Indels    0;  Gaps    0;

Qy           1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
               |||||||||||||||:|||||: ||:||| :||||:|||||||| ||||:|||||||||
Db           1 MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQ 60

Qy          61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
               ||| ||||||||||||||||||||||||||||||||||||||||||||||| | |
Db          61 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASRKTS 120

Qy         121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               ||| |||||||||||||:|||||||||||||||||||||||||||||||||| |||||
Db         121 FMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTV 180

Qy         181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               || ||||||||||||||||||||||||||:|||||||:|
Db         181 PQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNAS 222


RESULT 3
I12A_HORSE
ID   I12A_HORSE     STANDARD;      PRT;   222 AA.
AC   Q9XSQ6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20009534; PubMed=10541814;
RA   Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA   Argyle D.J., Onions D.E.;
RT   "Cloning and sequencing of horse interleukin-12 and interleukin-18
RT   cDNAs.";
RL   Immunogenetics 50:94-97(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; Y11130; CAA72012.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD    42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ   SEQUENCE   222 AA;  24800 MW;  5AD6DA874CE7AD2A CRC64;

  Query Match             85.7%;  Score 967;  DB 1;  Length 222;
  Best Local Similarity   84.7%;  Pred. No. 9.2e-77;
  Matches  188;  Conservative   15;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              |||||||||| |||||:|||||: ||:||||:| ||:|||||||||||| ||||||||||
Db          1 MCPPRGLLLVAILVLLNHLDHLSLARNLPTATPGPGMFQCLNHSQNLLRTVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| |||||||||||||||:||| |||||||  |||||||||| |||||||  ||||
Db         61 TLEFYSCTSEEIDHEDITKDKSSTVAACLPLELAPNESCLASREISFITNGSCLTPGKAS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               |  |||||||||||||:|||||||||:||:||||||:|||||||:|:|||||| ||
Db        121 SMMTLCLSSIYEDLKMYQVEFKAMNAKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||| |||  ||||||:|||||||||||||||:||| |||:|
Db        181 PQKPSLEGLDFYKTKVKLCILLHAFRIRAVTINRMMGYLNAS 222


RESULT 4
I12A_PIG
ID   I12A_PIG       STANDARD;      PRT;   222 AA.
AC   Q29053;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97383978; PubMed=9239844;
RA   Foss D.L., Murtaugh M.P.;
RT   "Molecular cloning and mRNA expression of porcine interleukin-12.";
RL   Vet. Immunol. Immunopathol. 57:121-134(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; L35765; AAA73897.1; ALT_INIT.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   222 AA;  24945 MW;  027D04411333AC94 CRC64;

  Query Match             85.1%;  Score 960;  DB 1;  Length 222;
  Best Local Similarity   84.7%;  Pred. No. 3.7e-76;
  Matches  188;  Conservative   12;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||| ||||:|||||: |||| : ||:|:||||||||:|||||||||:|
Db          1 MCPLRNLLLVATLVLLNHLDHLSLGRSLPATTAGPGMFKCLNHSQNLLKAVSNTLQKAKQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| ||||||||||||||||||||||||||  ||||||:|| ||||||:|| ||| |
Db         61 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLAARETSLITNGNCLTSGKTS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| |||||||||||| :||:|||||||||||||||||||||||| ||:||||||| ||
Db        121 FMTTLCLSSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQNMLTAITELMQALNFNSETV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||| |||| ||||||||||||||||||||||||||||||||
Db        181 PQKPSLEELDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222


RESULT 5
I12A_HUMAN
ID   I12A_HUMAN     STANDARD;      PRT;   219 AA.
AC   P29459; Q96QZ1;
DT   01-APR-1993 (Rel. 25, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35) (NK cell stimulatory
DE   factor chain 1) (NKSF1).
GN   IL12A OR NKSF1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91239523; PubMed=1674604;
RA   Gubler U., Chua A.O., Schoenhaut D.S., Dwyer C.M., McComas W.,
RA   Motyka R., Nabavi N., Wolitzky A.G., Quinn P.M., Familletti P.C.,
RA   Gately M.K.;
RT   "Coexpression of two distinct genes is required to generate secreted
RT   bioactive cytotoxic lymphocyte maturation factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4143-4147(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91201875; PubMed=1673147;
RA   Wolf S.F., Temple P.A., Kobayashi M., Young D., Dicig M., Lowe L.,
RA   Dzialo R., Fitz L., Ferenz C., Hewick R.M., Kelleher K.,
RA   Herrmann S.H., Clark S.C., Azzoni L., Chan S.H., Trinchieri G.,
RA   Perussia B.;
RT   "Cloning of cDNA for natural killer cell stimulatory factor, a
RT   heterodimeric cytokine with multiple biologic effects on T and
RT   natural killer cells.";
RL   J. Immunol. 146:3074-3081(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 23-48.
RX   MEDLINE=90370873; PubMed=2204066;
RA   Stern A.S., Podlaski F.J., Hulmes J.D., Pan Y.C.E., Quinn P.M.,
RA   Wolitzky A.G., Familletti P.C., Stremlo D.L., Truitt T.,
RA   Chizzonite R., Gately M.K.;
RT   "Purification to homogeneity and partial characterization of
RT   cytotoxic lymphocyte maturation factor from human B-lymphoblastoid
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6808-6812(1990).
RN   [5]
RP   SIMILARITY TO IL-6.
RX   MEDLINE=92247293; PubMed=1374259;
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RA   Merberg D.M., Wolf S.F., Clark S.C.;
RT   "Sequence similarity between NKSF and the IL-6/G-CSF family.";
RL   Immunol. Today 13:77-78(1992).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
CC       T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC.
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS. NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE
CC       RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M65271; AAA35694.1; -.
DR   EMBL; M65291; AAA59937.1; ALT_INIT.
DR   EMBL; AF404773; AAK84425.1; -.
DR   PIR; A39359; A39359.
DR   PIR; A36055; A36055.
DR   Genew; HGNC:5969; IL12A.
DR   MIM; 161560; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     22
FT   CHAIN       23    219       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     96     96       INTERCHAIN (PROBABLE).
FT   CARBOHYD     93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    213    213       M -> T (IN REF. 1).
SQ   SEQUENCE   219 AA;  24874 MW;  7C658AB7716112B2 CRC64;

  Query Match             83.4%;  Score 940.5;  DB 1;  Length 219;
  Best Local Similarity   84.2%;  Pred. No. 1.8e-74;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||| ||| |||| |: ||:|| |:| ||:| ||:||||||||||| ||||||
Db          1 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | |||||||||||||||||||||||||||||| ||||| ||| | |||||||| | |
Db         58 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  |||||||||||||:||| |||||||||||||||||||  ||||:||||||| ||
Db        118 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              |||||||||||||||||||||||||||||||||:|||||:|
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 219


RESULT 6
I12A_CEREL
ID   I12A_CEREL     STANDARD;      PRT;   221 AA.
AC   Q28233;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99304506; PubMed=10376218;
RA   Lockhart E., Slobbe L., Buchan G.;
RT   "The characterisation of a cervine immunoregulatory cytokine,
RT   interleukin 12.";
RL   DNA Seq. 10:139-148(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U57751; AAB02257.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    221       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD    41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   221 AA;  24899 MW;  5125E84A53C388DC CRC64;

  Query Match             80.8%;  Score 911.5;  DB 1;  Length 221;
  Best Local Similarity   82.4%;  Pred. No. 5.8e-72;
  Matches  183;  Conservative   11;  Mismatches   27;  Indels    1;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||:: |||| || ||:  |||| : ||   |||:||||||||:|||||||
Db          1 MCPLRSLLLLSTLVLLHHLPHLSLGRSLPPTTAGPG-RSCLNYSQNLLRAVSDTLQKARQ 59

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| |||||||||||||||||||||||||||||  ||||| ||| ||||:|||||||| |
Db         60 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLVSRETSLITHGSCLASGKTS 119

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| ||| |||||||||  |||:|||||||||||||||||||| || ||:||||||| ||
Db        120 FMTTLCLKSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQNMLAAIAELMQALNFNSETV 179

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||| |||| |||||:|||||||||||||||||||||||:||
Db        180 PQKPSLEEMDFYKTKVKLCILLHAFRIRAVTIDRMMSYLSSS 221


RESULT 7
I12A_SHEEP
ID   I12A_SHEEP     STANDARD;      PRT;   221 AA.
AC   Q9TU27; Q9MYU0;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A OR IL12P35.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
```

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RN   [1]
RP   SEQUENCE FROM N.A., AND SUBUNIT.
RC   TISSUE=Kidney;
RX   MEDLINE=20480126; PubMed=11023671;
RA   Swinburne S.J., Russ G.R., Krishnan R.;
RT   "Ovine interleukin 12 has biological activity on ovine and human
RT   activated peripheral blood mononuclear cells.";
RL   Cytokine 12:1546-1552(2000).
RN   [2]
RP   SEQUENCE OF 72-132 FROM N.A.
RX   MEDLINE=20539119; PubMed=11086544;
RA   Schmidt P., Kuehn C., Kang'a S., Hanotte O., Vanselow J., Anton I.,
RA   Langner C., Schwerin M.;
RT   "Interleukin-12 p35 encoding gene of cattle and sheep harbours a
RT   polymorphic T stretch in intron 4.";
RL   Anim. Genet. 31:283-285(2000).
CC   -!- FUNCTION: Cytokine that can act as a growth factor for activated T
CC       and NK cells, enhance the lytic activity of NK/lymphokine-
CC       activated Killer cells, and stimulate the production of IFN-gamma
CC       by resting PBMC (By similarity).
CC   -!- SUBUNIT: Disulfide-bonded heterodimer of 40 kDa and 35 kDa
CC       subunits.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF173557; AAD51976.1; -.
DR   EMBL; AJ271035; CAB97178.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal; Glycoprotein.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    221       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD    95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   221 AA;  24859 MW;  9E9A2300914E4167 CRC64;

  Query Match             80.7%;  Score 910.5;  DB 1;  Length 221;
  Best Local Similarity   81.5%;  Pred. No. 7.1e-72;
  Matches  181;  Conservative   14;  Mismatches   26;  Indels    1;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||:: |||| || ||:  ||||| :  ||   ||::||||||||||||||||
Db          1 MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTAGPGT-SCLDYSQNLLRAVSNTLQKARQ 59

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| ||||||||||||||||||||||||||||  |||||||| |||||| ||:||| |
Db         60 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRETSLITNGHCLSSGKTS 119

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| ||| |||:||||| |||:|||||||||||||:||||||| || ||:|||||:| ||
Db        120 FMTTLCLRSIYKDLKMYHMEFQAMNAKLLMDPKRQVFLDQNMLAAIAELMQALNFDSETV 179

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||| |||| ||||||:||||||||||||||||||||:||
Db        180 PQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYLSSS 221


RESULT 8
I12A_BOVIN
ID   I12A_BOVIN     STANDARD;      PRT;   221 AA.
AC   P54349;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Holstein; TISSUE=Lymphoid;
RX   MEDLINE=95244628; PubMed=7727547;
RA   Zarlenga D.S., Canals A., Aschenbrenner R.A., Gasbarre L.C.;
RT   "Enzymatic amplification and molecular cloning of cDNA encoding the
RT   small and large subunits of bovine interleukin 12.";
RL   Biochim. Biophys. Acta 1270:215-217(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U14416; AAA85810.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    221       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD    95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   221 AA;  24944 MW;  0462DEE9DD33BC90 CRC64;

  Query Match             80.5%;  Score 908.5;  DB 1;  Length 221;
  Best Local Similarity   82.0%;  Pred. No. 1.1e-71;
  Matches  182;  Conservative   13;  Mismatches   26;  Indels    1;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||:: |||| || ||:  ||||| : |||   ||::||||||||||||||||
Db          1 MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPG-RSCLDYSQNLLRAVSNTLQKARQ 59

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| ||||||||||||||||||||||||||||  |||||||| | |||| ||||||
Db         60 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRETSFITNGHCLASGKTS 119

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| ||| |||||||||| :||:||||||||||||||||||| || ||:|||||:| ||
Db        120 FMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQNMLAAIAELMQALNFDSETV 179

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||| ||:| ||||||:||||||||||||||||||||:||
Db        180 PQKPSLKELDFYKTKVKLCILLHAFRIRAVTIDRMMSYLSSS 221


RESULT 9
I12A_CAPHI
ID   I12A_CAPHI     STANDARD;      PRT;   221 AA.
AC   O02814;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
```

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OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Beyer J.C., Kumpula-Mcwhirter N.M., Cheevers W.P.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF003542; AAB61287.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    221       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD    95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   221 AA;  24832 MW;  58031AAD87199357 CRC64;

  Query Match             79.2%;  Score 893.5;  DB 1;  Length 221;
  Best Local Similarity   80.6%;  Pred. No. 2.1e-70;
  Matches  179;  Conservative   14;  Mismatches   28;  Indels    1;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||:: |||| || ||:  |||| :  ||   ||::||||||||||||||||||
Db          1 MCPLRSLLLISTLVLLHHLPHLSLGRSLPITTAGPG-RSCLDYSQNLLRAVSNTLQKARQ 59

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| ||||||||||||||||||||||||||||  ||||||||| |||||| |||||| |
Db         60 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRETSLITNGHCLASGKTS 119

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||| ||| |||:||||| |||:|:|||||||||: |||||| || ||:|||||:| ||
Db        120 FMTTLCLRSIYKDLKMYHMEFQAINAKLLMDPKRQVSLDQNMLAAIAELMQALNFDSETV 179

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||| |||| ||||||:|||||||||||||||||||||:||
Db        180 PQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYLSSS 221


RESULT 10
I12A_MACMU
ID   I12A_MACMU     STANDARD;      PRT;   219 AA.
AC   P48091;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19842; AAA86707.1; ALT_INIT.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    219       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    96     96       INTERCHAIN (PROBABLE).
FT   CARBOHYD    24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   219 AA;  24904 MW;  D676D8B6663C4A33 CRC64;

  Query Match             78.8%;  Score 888.5;  DB 1;  Length 219;
  Best Local Similarity   80.2%;  Pred. No. 5.6e-70;
  Matches  178;  Conservative   12;  Mismatches   29;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||:|: ||:|  |:| | :| ||:|||||||:| |||||||||
Db          1 MCPARSLLLVATLVL---LDYLSLARNLSVATPGPEMFPCLHHSQNLLKAASNTLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              || | |||||||||||||||||||||||||||  |||| ||| | ||||||||| | |
Db         58 ILEFYPCTSEEIDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              || ||| ||||||||||:||| |||||| ||||||||||:|  ||||:|||||| ||
Db        118 FMMALCLRSIYEDLKMYQVEFKTMNAKLLRDPKRQIFLDQNILGVIDELMQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||:|||||:|
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 219


RESULT 11
I12A_CERTO
ID   I12A_CERTO     STANDARD;      PRT;   219 AA.
AC   P46661;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U19835; AAA86702.1; ALT_INIT.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    219       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    96     96       INTERCHAIN (PROBABLE).
FT   CARBOHYD    24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   219 AA;  24801 MW;  844770181AC771BF CRC64;

  Query Match             78.3%;  Score 883.5;  DB 1;  Length 219;
  Best Local Similarity   79.3%;  Pred. No. 1.5e-69;
  Matches  176;  Conservative   15;  Mismatches   28;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||| ||| |  ||:|: ||:|  |:| | :| ||:||||||:|  ||||||||
Db          1 MCPARSLLLVATLVL---LDYLSLARNLSVATPGPEMFPCLHHSQNLLKAACNTLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              || | ||||||||||||||||||||||||||  |||||  ||| |:|||||||| | |
Db         58 ILEFYPCTSEEIDHEDITKDKTSTVEACLPLELIKNESCLNSRETSVITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  ||| |||||||:||:||| |||||||||||||||||:|  ||||:||||||| ||
Db        118 FMMALCLRSIYEDLKIYQVEFKTMNAKLLMDPKRQIFLDQNILGVIDELMQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              |||||||||||||||||||||||:||||||||:|||||:|
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFKIRAVTIDRVMSYLNAS 219


RESULT 12
I12A_MARMO
ID   I12A_MARMO     STANDARD;      PRT;   223 AA.
AC   Q61728;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Laxton C.D., Foster G.R., Shanmuganathan S., Mills J.S.,
RA   Ackrill A.M.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97018; CAA65746.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     23       BY SIMILARITY.
FT   CHAIN       24    223       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD    41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   121    121       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   176    176       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   223 AA;  24833 MW;  2421024F5A4FFD14 CRC64;

  Query Match             56.4%;  Score 636.5;  DB 1;  Length 223;
  Best Local Similarity   59.3%;  Pred. No. 3.7e-48;
  Matches  134;  Conservative   32;  Mismatches   53;  Indels    7;  Gaps    4;

Qy          1 MCP-PRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQ-CLNHSQNLLRAVSNTLQKA 58
              ||| | |||:  |||| ||     ||:|| ::| | : | | | || ||  | : || |
Db          1 MCPSARSLLLLASLVLLEHLGS---ARNLPRSTPVPAVSQECHNLSQTLLSTVDSALQNA 57

Qy         59 RQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGK 118
              : || | |::||::|||||||::|:||:|||| ||  ||:|||||| | |   | | ||:
Db         58 IEILEYYPCSAEEVNHEDITKNRTNTVKACLPQELAQNENCLASRETSFIIKRSSLTSGR 117

Qy        119 ASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSV 178
              |: | || ||||||||||:| ||:: |||||| ||: |: :| |:| |:||:| |:
Db        118 TSWNTTLCFSSIYEDLKMYQLELKAISEKLLMDPKGQIYEDKALLAAVDYLMQAVNVNNE 177

Qy        179 TVPQKSSLEEP--DFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||  | | |  : |:|| |||||||| |||||||:|:|||||||
Db        178 TVPQTPSPEAPSSNLYRTKTKLCILLHALRIRAVTINRVMSYLNSS 223


RESULT 13
I12A_MOUSE
ID   I12A_MOUSE     STANDARD;      PRT;   215 AA.
AC   P43431;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
```

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RX   MEDLINE=92268481; PubMed=1350290;
RA   Schoenhaut D.S., Chua A.O., Wolitzky A.G., Quinn P.M., Dwyer C.M.,
RA   Gately M.K., Gubler U.;
RT   "Cloning and expression of murine IL-12.";
RL   J. Immunol. 148:3433-3440(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96257799; PubMed=8647196;
RA   Tone Y., Thompson S.A., Babik J.M., Nolan K.F., Tone M., Raven C.,
RA   Waldmann H.;
RT   "Structure and chromosomal location of the mouse interleukin-12 p35
RT   and p40 subunit genes.";
RL   Eur. J. Immunol. 26:1222-1227(1996).
RN   [3]
RP   SEQUENCE OF 1-5 FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=96144329; PubMed=8557982;
RA   Yoshimoto T., Kojima K., Funakoshi T., Endo Y., Fujita T.,
RA   Nariuchi H.;
RT   "Molecular cloning and characterization of murine IL-12 genes.";
RL   J. Immunol. 156:1082-1088(1996).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86672; AAA39292.1; -.
DR   EMBL; S82419; AAB37382.1; -.
DR   EMBL; S82412; AAB37382.1; JOINED.
DR   EMBL; S82414; AAB37382.1; JOINED.
DR   EMBL; S82417; AAB37382.1; JOINED.
DR   EMBL; S82418; AAB37382.1; JOINED.
DR   EMBL; D63334; BAA09647.1; -.
DR   MGD; MGI:96539; Il12a.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    215       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    92     92       INTERCHAIN (PROBABLE).
FT   CARBOHYD    89     89       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   215 AA;  24179 MW;  56845B9B66D35A53 CRC64;

  Query Match             52.4%;  Score 591.5;  DB 1;  Length 215;
  Best Local Similarity   54.5%;  Pred. No. 2.8e-44;
  Matches  121;  Conservative   36;  Mismatches   58;  Indels    7;  Gaps    2;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||  | || :  | |   |:||: || :| : |:    :||: |:|||:   : :: ||:
Db          1 MCQSRYLLFLATLAL---LNHLSLARVIPVSGPA----RCLSQSRNLLKTTDDMVKTARE 53

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
               |: ||||:|:|||||||:|:|||:: ||||||  ||||||:|| |  | ||||   |:|
Db         54 KLKHYSCTAEDIDHEDITRDQTSTLKTCLPLELHKNESCLATRETSSTTRGSCLPPQKTS 113

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              |  ||| ||||||||||| ||:|:|| |     :|| ||: || |||||:|:|| |  |:
Db        114 LMMTLCLGSIYEDLKMYQTEFQAINAALQNHNHQQIILDKGMLVAIDELMQSLNHNGETL 173

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
                ||  : | | |: |:|||||||||  | |||:|:| ||:|:

Db        174 RQKPPVGEADPYRVKMKLCILLHAFSTRVVTINRVMGYLSSA 215


RESULT 14
FAS_HUMAN
ID   FAS_HUMAN      STANDARD;      PRT;  2504 AA.
AC   P49327;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fatty acid synthase (EC 2.3.1.85) [Includes: EC 2.3.1.38; EC 2.3.1.39;
DE   EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14].
GN   FASN OR FAS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96004605; PubMed=7567999;
RA   Jayakumar A., Tai M.-H., Huang W.-Y., Al-Feel W., Hsu M.,
RA   Abu-Elheiga L., Chirala S.S., Wakil S.J.;
RT   "Human fatty acid synthase: properties and molecular cloning.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:8695-8699(1995).
RN   [2]
RP   SEQUENCE OF 753-758 AND 1285-1297.
RX   MEDLINE=94294385; PubMed=8022791;
RA   Kuhajda F.P., Jenner K., Wood F.D., Hennigar R.A., Jacobs L.B.,
RA   Dick J.D., Pasternack G.R.;
RT   "Fatty acid synthesis: a potential selective target for
RT   antineoplastic therapy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:6379-6383(1994).
CC   -!- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
CC       LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
CC       THIS MULTIFUNCTIONAL PROTEIN HAS 7 CATALYTIC ACTIVITIES AND AN
CC       ACYL CARRIER PROTEIN.
CC   -!- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a
CC       long-chain fatty acid + (N+1) CoA + N CO(2) + 2N NADP(+).
CC   -!- CATALYTIC ACTIVITY: Acetyl-CoA + [acyl-carrier protein] = CoA +
CC       acetyl-[acyl-carrier protein].
CC   -!- CATALYTIC ACTIVITY: Malonyl-CoA + [acyl-carrier protein] = CoA +
CC       malonyl-[acyl-carrier protein].
CC   -!- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
CC       carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
CC       [acyl-carrier protein].
CC   -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC       NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC   -!- CATALYTIC ACTIVITY: (3R)-3-hydroxypalmitoyl-[acyl-carrier protein]
CC       = 2-hexadecenoyl-[acyl-carrier protein] + H(2)O.
CC   -!- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADP(+) = trans-
CC       2,3-dehydroacyl-[acyl-carrier protein] + NADPH.
CC   -!- CATALYTIC ACTIVITY: Oleoyl-[acyl-carrier protein] + H(2)O = [acyl-
CC       carrier protein] + oleate.
CC   -!- SUBUNIT: HOMODIMER, WHICH IS ARRANGED IN A HEAD TO TAIL FASHION.
CC   -!- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN BRAIN, LUNG, AND
CC       LIVER.
CC   -!- MISCELLANEOUS: THE RELATIVELY LOW BETA-KETOACYL SYNTHASE ACTIVITY
CC       MAY BE ATTRIBUTABLE TO THE LOW 4'-PHOSPHOPANTETHEINE CONTENT OF
CC       THE PROTEIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U26644; AAC50259.1; -.
DR   Genew; HGNC:3594; FASN.
DR   MIM; 600212; -.
DR   InterPro; IPR001227; Ac_transferase.
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DR   InterPro; IPR002085; Adh_zn_family.
DR   InterPro; IPR000794; Ketoacyl-synt.
DR   InterPro; IPR003880; Ppantne_attach.
DR   InterPro; IPR000051; SAM_bind.
DR   InterPro; IPR001031; Thioesterase.
DR   Pfam; PF00107; adh_zinc; 1.
DR   Pfam; PF00109; ketoacyl-synt; 1.
DR   Pfam; PF00550; pp-binding; 1.
DR   Pfam; PF00698; Acyl_transf; 1.
DR   Pfam; PF00975; Thioesterase; 1.
DR   Pfam; PF02801; ketoacyl-synt_C; 1.
DR   PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR   PROSITE; PS50075; ACP_DOMAIN; 1.
KW   Fatty acid biosynthesis; Multifunctional enzyme; Phosphopantetheine;
KW   Hydrolase; Oxidoreductase; Transferase; Lyase; NADP;
KW   Pyridoxal phosphate.
FT   DOMAIN        1    413       BETA-KETOACYL SYNTHASE.
FT   DOMAIN      428    815       ACYL AND MALONYL TRANSFERASES.
FT   DOMAIN     1630   1857       ENOYL REDUCTASE.
FT   DOMAIN     1858   2113       BETA-KETOACYL REDUCTASE.
FT   DOMAIN     2118   2174       ACYL CARRIER (ACP).
FT   DOMAIN     2202   2504       THIOESTERASE.
FT   ACT_SITE    161    161       BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT   ACT_SITE    580    580       MALONYLTRANSFERASE (BY SIMILARITY).
FT   ACT_SITE    876    876       BETA-HYDROXYACYL DEHYDRATASE (BY
FT                                SIMILARITY).
FT   NP_BIND    1666   1683       NADP (ER).
FT   BINDING    1699   1699       PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT   NP_BIND    1880   1895       NADP (KR).
FT   BINDING    2151   2151       PHOSPHOPANTETHEINE (BY SIMILARITY).
FT   ACT_SITE   2302   2302       THIOESTERASE (BY SIMILARITY).
FT   ACT_SITE   2475   2475       THIOESTERASE (BY SIMILARITY).
SQ   SEQUENCE   2504 AA;  273100 MW;  8AAF9809B2338DFA CRC64;

  Query Match             8.6%;  Score 96.5;  DB 1;  Length 2504;
  Best Local Similarity   22.7%;  Pred. No. 4.4;
  Matches   60;  Conservative   34;  Mismatches   87;  Indels   83;  Gaps   13;

Qy          4 PRGLLLVTILVLLSHLDHLTW----ARSLP--TASPSPGIFQCLNHSQN---------- 46
              |||  |:: |:   |   | |    |   |  : |||  |: |   |::
Db        822 PRGTPLISPLIKWDH--SLAWDAPAAEDFPNGSGSPSATIYTCTPSSESPDRYLVDHTID 879

Qy         47 ---------LLRAVSNTLQKARQTLELYSCTSEE-IDHEDITKDKTSTVEACLPLELTMN 96
                      |  |  || :|   ||      |: : |:     || ||     ||: :
Db        880 GRVLFPATGYLSIVWKTLARAWAGLEQLPVVFEDVVQHQATILPKTGTVS----LEVRLL 935

Qy         97 ESCLASREISLITNGSCLASGKA----------------------SFMTVLCLSSIYEDL 134
              |   |:    :  }|: : |||                          |  : :|::|
Db        936 E---ATGAFEVSENGNLVVSGKVYQWDDPDPRLFDHPESPHPNSPRSPLFLAQAEVYKEL 992

Qy        135 KM----YQMEFKA-MNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEP 189
              ::    |   |:  : | |  |  | :: | | :: :| :||     |:    |  |  |
Db        993 RLRGYDYGPHFQGILEASLEGDSGRLLWKD-NWVSFMDTMLQM----SILGSAKHGLYLP 1047

Qy        190 DFYKTKIKLCILLHAFRIRAVTID 213
                          |: |: ||
Db       1048 T---------------RVTAIHID 1056


RESULT 15
YD86_SCHPO
ID   YD86_SCHPO     STANDARD;      PRT;  1957 AA.
AC   Q10411;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Hypothetical protein C1F3.06c in chromosome I.
GN   SPAC1F3.06C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z70690; CAA94624.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   1957 AA;  222785 MW;  3F480CA06171D9DA CRC64;

  Query Match             7.8%;  Score 87.5;  DB 1;  Length 1957;
  Best Local Similarity   20.7%;  Pred. No. 20;
  Matches   51;  Conservative   51;  Mismatches   87;  Indels   57;  Gaps    9;

Qy          8 LLVTILVLLSHLDHLTWARSLPTASPSPGIFQCL-NHSQNLLRAVSNTLQKARQTLELYS 66
              |:  |  : | ||  ::   | :|    |  | | : | :|:  : : ||:|:: :::
Db       1458 LMEKIESINSSLDDKSF--ELASAVEKLGALQKLHSESLSLMENIKSQLQEAKEKIQVDE 1515

Qy         67 CTSEEIDHE----------------DITKDKTSTVEA---CLPLELTMNESCLASREISL 107
                | :|:|||                | :| :  :|     |  | :  :     :|  :
Db       1516 STIQELDHEITASKNNYEGKLNDKDSIIRDLSENIEQLNNLLAEEKSAVKRLSTEKESEI 1575

Qy        108 ITNGSCLAS------------GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQ 155
              :   | ||             |::    | |:|  |:|:: : |  ::  ::| | : |
Db       1576 LQFNSRLADLEYHKSQVESELGRSK----LKLASTTEELQLAENERLSLTTRML-DLQNQ 1630

Qy        156 IFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRM 215
              :    |:  :: | |: |           |||:         :  |    :|:: |:: :
Db       1631 VKDLSNIKDSLSEDLRTLR----------SLED--------SVASLQKECKIKSNTVESL 1672

Qy        216 MSYLNS 221
                | |
Db       1673 QDVLTS 1678


Search completed: July 15, 2003, 11:06:59
Job time : 6.86517 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:57:19 ; Search time 19.6722 Seconds
(without alignments)
2325.231 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	940.5	83.4	253	4	O60595	O60595 homo sapien
2	793.5	70.3	221	11	Q924V6	Q924v6 cavia porce
3	677.5	60.1	215	11	Q91ZK6	Q91zk6 sigmodon hi
4	632.5	56.1	223	11	Q9ET04	Q9et04 marmota mon
5	607.5	53.9	215	11	Q9R103	Q9r103 rattus norv
6	540	47.9	210	11	Q924K6	Q924k6 meriones un
7	441	39.1	94	6	O62777	O62777 felis silve
8	272	24.1	61	6	Q9MYW1	Q9myw1 bos taurus
9	270.5	24.0	116	11	Q9QUT1	Q9qut1 mus musculu
10	98.5	8.7	444	4	Q9NXJ6	Q9nxj6 homo sapien
11	97.5	8.6	816	10	Q9SJT3	Q9sjt3 arabidopsis
12	93	8.2	1583	16	Q92GE9	Q92ge9 rickettsia
13	92.5	8.2	539	4	Q9HCC8	Q9hcc8 homo sapien
14	90	8.0	537	5	Q9VZU0	Q9vzu0 drosophila
15	90	8.0	581	10	O04143	O04143 silene lati
16	90	8.0	615	5	Q18809	Q18809 caenorhabdi
17	89.5	7.9	243	15	P89806	P89806 human immun
18	89.5	7.9	383	16	O84156	O84156 chlamydia t
19	89.5	7.9	498	15	Q9QML3	Q9qml3 human immun
20	89.5	7.9	1433	15	Q9QML4	Q9qml4 human immun
21	89	7.9	547	2	Q8RJP4	Q8rjp4 alteromonas
22	88.5	7.8	276	15	Q992Q5	Q992q5 human immun
23	88	7.8	215	15	Q8US99	Q8us99 human immun
24	87.5	7.8	211	15	Q8US97	Q8us97 human immun
25	87.5	7.8	243	15	P89800	P89800 human immun
26	87.5	7.8	243	15	P89814	P89814 human immun
27	87.5	7.8	273	4	Q9Y448	Q9y448 homo sapien
28	87.5	7.8	489	15	Q80307	Q80307 human immun
29	87.5	7.8	498	15	P88150	P88150 human immun
30	87.5	7.8	1433	15	P90071	P90071 human immun
31	87	7.7	488	10	Q948S0	Q948s0 athyrium yo
32	86.5	7.7	488	15	Q79362	Q79362 human immun
33	86.5	7.7	495	15	Q90VT4	Q90vt4 human immun
34	86.5	7.7	924	5	O15738	O15738 dictyosteli
35	86.5	7.7	1430	15	Q90VT5	Q90vt5 human immun
36	86	7.6	446	10	Q9M0E1	Q9m0e1 arabidopsis
37	86	7.6	1286	5	Q21025	Q21025 caenorhabdi
38	85.5	7.6	143	15	Q97286	Q97286 human immun
39	85.5	7.6	243	15	P89802	P89802 human immun
40	85.5	7.6	489	15	Q80305	Q80305 human immun
41	85.5	7.6	498	15	Q9Q6G9	Q9q6g9 human immun
42	85.5	7.6	849	16	Q97E36	Q97e36 clostridium
43	85.5	7.6	5303	5	Q9V628	Q9v628 drosophila
44	85	7.5	240	15	Q9IM34	Q9im34 human immun
45	85	7.5	261	15	Q8Q3X7	Q8q3x7 human immun

ALIGNMENTS

RESULT 1
O60595
ID O60595 PRELIMINARY; PRT; 253 AA.
AC O60595;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin 12 (Interleukin-12 P35 subunit).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Guo Y., Wu M.;
RT "Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
RT Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-39 FROM N.A.
RC TISSUE=PLACENTA;
RA Hayes M.P., Murphy F.J., Burd P.R.;
RL Blood 0:0-0(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Hongyuan J., Meiyun Z.;
RT "Cloning and sequence analysis of IL-12 cDNA from Chinese.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF101062; AAD16432.1; -.
DR EMBL; AF050083; AAC05211.1; -.
DR EMBL; AF180562; AAD56385.1; -.
DR InterPro; IPR002106; AAtRNA_ligaseII.
DR InterPro; IPR004281; IL12.
DR Pfam; PF03039; IL12; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
FT VARIANT 247 247 M -> T.
SQ SEQUENCE 253 AA; 28293 MW; FAC56ACD2A620BD5 CRC64;

Query Match 83.4%; Score 940.5; DB 4; Length 253;

```
  Best Local Similarity   84.2%;  Pred. No. 5.7e-79;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||| ||| |||| |:|| |:| ||:| ||:|||||||||||| ||||||
Db         35 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 91

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | ||||||||||||||||||||||||||| ||||| ||| | |||||||| | |
Db         92 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 151

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  |||||||||||||:||| |||||||||||||||||||  ||||:|||||| ||
Db        152 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 211

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||||:|||||:|
Db        212 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 253


RESULT 2
Q924V6
ID   Q924V6      PRELIMINARY;      PRT;   221 AA.
AC   Q924V6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p35 subunit (IL-12 p35).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HARTLEY;
RA   Shiratori I., Matsumoto M., Tsuji S., Nomura M., Toyoshima K.,
RA   Seya T.;
RT   "Molecular cloning and functional characterization of guinea pig
RT   Interleukin -12.";
RL   Int. Immunol. 0:0-0(2001).
DR   EMBL; AB025723; BAB63962.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SQ   SEQUENCE   221 AA;  24687 MW;  972E59F5A11DE896 CRC64;

  Query Match           70.3%;  Score 793.5;  DB 11;  Length 221;
  Best Local Similarity   73.2%;  Pred. No. 1.8e-65;
  Matches  164;  Conservative   19;  Mismatches   36;  Indels    5;  Gaps    2;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGI--FQCLNHSQNLLRAVSNTLQKA 58
              | | |  ||:| ||||      : ||:|| |||:|     || |||| |||||:: | ||
Db          1 MSPLRKCLLLTSLVLLV---SCSLARNLPRASPAPVTEPVQCFNHSQTLLRAVNSELHKA 57

Qy         59 RQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGK 118
               | | :|||| ||||||||||||||||:||:|||| |||||| || ||||||||||
Db         58 IQMLAVYSCTPEEIDHEDITKDKTSTVKACVPLELVKNESCLASGHISFTTNGSCLASGK 117

Qy        119 ASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSV 178
               |||  |||:|||||||:||:||| |||:|||||:||||||||||:|||||:|||| : |
Db        118 TSFMMALCLNSIYEDLKLYQLEFKNMNAQLLMDPQRQIFLDQNMLSAIDELIQALNGSDV 177

Qy        179 TVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||| ||||||||| |:||||||||||||||||:]||| ||
Db        178 TVPQKLSLEEPDFYKIKMKLCILLHAFRIRAVTIDRVMSYLTSS 221


RESULT 3
Q91ZK6
ID   Q91ZK6      PRELIMINARY;      PRT;   215 AA.
AC   Q91ZK6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin 12 p35 subunit.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Blanco J.C., Pletneva L.M., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF421396; AAL16937.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   215 AA;  24042 MW;  435DF86A7D72A244 CRC64;

  Query Match           60.1%;  Score 677.5;  DB 11;  Length 215;
  Best Local Similarity   63.5%;  Pred. No. 9.2e-55;
  Matches  141;  Conservative   26;  Mismatches   48;  Indels    7;  Gaps    2;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||  | ||    |  |: | ||: ||: | ::|:    ||| |||||||  :: |:|| |
Db          1 MCSSRCLL---FLATLAFLIHLSLARATPVSTPA----QCLAHSQNLLRTTNHMLEKAIQ 53

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||: | ||:|:|||||||:|||||: |||| ||  |||| || : | :| ||||   | |
Db         54 TLKHYPCTAEDIDHEDITEDKTSTLNACLPPELAKNESCWASGKTSSVTRGSCLPPQKTS 113

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               |  ||||||||||||| ||||:||:||   ::|| ||:|||||||||:|||| |  |
Db        114 SMMTLCLSSIYEDLKMYQTEFKAINAELLDHNRKQIILDENMLTAIDELMQALNLNGETR 173

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||| |||| | || |||||||||| |||:||:|:|||||||:
Db        174 PQKPSLEEADPYKVKIKLCILLHAFSIRAITINRVMSYLNSA 215


RESULT 4
Q9ET04
ID   Q9ET04      PRELIMINARY;      PRT;   223 AA.
AC   Q9ET04;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-12 p35 subunit.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21424491; PubMed=11533170;
RA   Garcia-Navarro R., Blanco-Urgoiti B., Berraondo P.,
RA   Sanchez De La Rosa R., Vales A., Hervas-Stubbs S., Lasarte J.J.,
RA   Borras F., Ruiz J., Prieto J.;
RT   "Protection against Woodchuck Hepatitis Virus (WHV) Infection by Gene
RT   Gun Coimmunization with WHV Core and Interleukin-12.";
RL   J. Virol. 75:9068-9076(2001).
DR   EMBL; AF288520; AAG01024.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   223 AA;  24831 MW;  2423E5498A4FFD14 CRC64;

  Query Match           56.1%;  Score 632.5;  DB 11;  Length 223;
  Best Local Similarity   58.8%;  Pred. No. 1.4e-50;
  Matches  133;  Conservative   32;  Mismatches   54;  Indels    7;  Gaps    4;

Qy          1 MCP-PRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQ-CLNHSQNLLRAVSNTLQKA 58
              |||  | |||:  |||| ||     ||:|| ::| | : | | | .|| ||  | : || |
Db          1 MCPSARSLLLLASLVLLEHLGS---ARNLPRSTPVPAVSQECHNLSQTLLSTVDSALQNA 57
```

```
Qy          59 RQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGK 118
               : || | |::||::|||||||::|:||:|||| ||  ||:|||||| | |   | | ||:
Db          58 IEILEYYPCSAEEVNHEDITKNRTNTVKACLPQELAQNENCLASRETSFIIKRSSLTSGR 117

Qy         119 ASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSV 178
               |: | || |||||||||||:| ||:: ||||||| ||: |: :| |:| |:||:| |:
Db         118 TSWNTTLCFSSIYEDLKMYQLELKAISEKLLMDPKGQIYEDKALLAAVDYLMQAVNVNNE 177

Qy         179 TVPQKSSLE--EPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               ||||  | |   |: |:|| |||||||| |||||| :|:|||||||
Db         178 TVPQTPSPEAPSPNLYRTKTKLCILLHALRIRAVTTNRVMSYLNSS 223


RESULT 5
Q9R103
ID   Q9R103      PRELIMINARY;      PRT;   215 AA.
AC   Q9R103;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 p35 subunit.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DA;
RA   Verma N.D., He X.Y., Hall B.M.;
RT   "Cloning of the rat interleukin 12 p35 subunit.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177031; AAD51364.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   215 AA;  24246 MW;  60EDC00C70F0E005 CRC64;

  Query Match             53.9%;  Score 607.5;  DB 11;  Length 215;
  Best Local Similarity   56.3%;  Pred. No. 2.7e-48;
  Matches  125;  Conservative   36;  Mismatches   54;  Indels    7;  Gaps    2;

Qy           1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
               ||  | || :  |||   |:||| || :| : |:    :||| |||||:   : :: ||:
Db           1 MCQSRYLLFLATLVL---LNHLTSARVIPVSGPA----KCLNQSQNLLKTTDDMVRTARE 53

Qy          61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
               |: |||: :|||||||:|||||:|||||||  ||||||::| | |  ||||   | |
Db          54 KLKHYSCTAGDIDHEDITRDKTSTLEACLPLELHKNESCLATKETSSIIRGSCLPPQKTS 113

Qy         121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               |  ||| |||||||||| ||:|:|| |     :|| ||:||| |||||:::|| :  |:
Db         114 LMMTLCLGSIYEDLKMYQSEFQAINAALQSHNHQQITLDRNMLMAIDELMRSLNHSGETL 173

Qy         181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               ||: : | | |: |:|||||||||  | :||:|:|:||:||
Db         174 HQKAPMGEADPYRVKMKLCILLHAFSTRVMTINRVMNYLSSS 215


RESULT 6
Q924K6
ID   Q924K6      PRELIMINARY;      PRT;   210 AA.
AC   Q924K6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-12 p35 subunit.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gaucher D., Chadee K.;
RT   "Molecular cloning of gerbil interleukin-12, and its expression as a
RT   bioactive single-chain protein.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288849; AAK83072.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   210 AA;  23742 MW;  5D44D9E2BFA0BB70 CRC64;

  Query Match             47.9%;  Score 540;  DB 11;  Length 210;
  Best Local Similarity   55.5%;  Pred. No. 4.5e-42;
  Matches  121;  Conservative   28;  Mismatches   57;  Indels   12;  Gaps    5;

Qy           5 RGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLEL 64
               | |  :  |||:    ||: ||: | : |:    :||| || |||   | |: ||| |
Db           5 RRLFFLVTLVLI----HLSLARAKPVSGPA----RCLNSSQTLLRTTDNALKTARQKLTN 56

Qy          65 YSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTV 124
               | | :|: | ||||||||||::|||||||  ||||||    |:|  ||||   | | |
Db          57 Y-CGAEDFDREDITKDKTSTLKACLPLELVKNESCLAGETSSMI-RGSCLLPQKTSSMMT 114

Qy         125 LCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKS 184
               |||||||||||:|| ||:|::|:|    : || ||::|| |||||:|||| |  |||:|
Db         115 LCLSSIYEDLKIYQTEFQAIDAELRR--QNQITLDKDMLAAIDELMQALNHNGQTVPRKP 172

Qy         185 SLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               | | |  | :: ||| |||| ||  ||:::|||||||
Db         173 YLAERDPIKLEMHLCIQLHAFSIRVTTINKVMSYLNSS 210


RESULT 7
O62777
ID   O62777      PRELIMINARY;      PRT;    94 AA.
AC   O62777;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 p35 subunit (Fragment).
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99322318; PubMed=10391845;
RA   Harley R., Helps C.R., Harbour D.A., Gruffydd-Jones T.J., Day M.J.;
RT   "Cytokine mRNA expression in lesions in cats with chronic
RT   gingivostomatitis.";
RL   Clin. Diagn. Lab. Immunol. 6:471-478(1999).
DR   EMBL; AF054605; AAC15978.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
FT   NON_TER       1      1
FT   NON_TER      94     94
SQ   SEQUENCE   94 AA;  10616 MW;  AD67866E916201AD CRC64;

  Query Match             39.1%;  Score 441;  DB 6;  Length 94;
  Best Local Similarity   92.6%;  Pred. No. 2.4e-33;
  Matches   87;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          47 LLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREIS 106
               ||||:|||| |||||| ||||||||||||||||||||||||||||||||||||||||||
Db           1 LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREIS 60

Qy         107 LITNGSCLASGKASFMTVLCLSSIYEDLKMYQME 140
               |||||||||| | |||| |||||||||||||:|
Db          61 LITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE 94


RESULT 8
Q9MYW1
ID   Q9MYW1      PRELIMINARY;      PRT;    61 AA.
AC   Q9MYW1;
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DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12 polypeptide 35 (Fragment).
GN   IL-12 P35.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20539119; PubMed=11086544;
RA   Schmidt P., Kuehn C., Kang'a S., Hanotte O., Vanselow J., Anton I.,
RA   Langner C., Schwerin M.;
RT   "Interleukin-12 p35 encoding gene of cattle and sheep harbours a
RT   polymorphic T stretch in intron 4.";
RL   Anim. Genet. 31:283-283(2000).
DR   EMBL; AJ271034; CAB97049.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
FT   NON_TER       1      1
FT   NON_TER      61     61
SQ   SEQUENCE   61 AA;  6699 MW;  9C32147DB2BFA1A4 CRC64;

  Query Match             24.1%;  Score 272;  DB 6;  Length 61;
  Best Local Similarity   86.9%;  Pred. No. 6e-18;
  Matches   53;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         73 DHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYE 132
              ||||||||||||||||||||  |||||||| | |||| |||||| |||| ||| ||||
Db          1 DHEDITKDKTSTVEACLPLELATNESCLASRETSFITNGHCLASGKTSFMTTLCLRSIYE 60

Qy        133 D 133
              |
Db         61 D 61


RESULT 9
Q9QUT1
ID   Q9QUT1      PRELIMINARY;      PRT;   116 AA.
AC   Q9QUT1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12A.
GN   IL12A OR LL12A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SJL/J, AND B10.S/J; TISSUE=SPLEEN;
RA   Ma R.Z., Teuscher C.;
RT   "Screening for candidate genes of mouse autoimmnue diseases.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF128211; AAF22552.1; -.
DR   EMBL; AF128210; AAF22551.1; -.
DR   MGD; MGI:96539; Il12a.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   116 AA;  12954 MW;  06777BF8D56AAAFE CRC64;

  Query Match             24.0%;  Score 270.5;  DB 11;  Length 116;
  Best Local Similarity   50.5%;  Pred. No. 1.8e-17;
  Matches   55;  Conservative   22;  Mismatches   25;  Indels    7;  Gaps    2;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||  | || :  | |   |:||: || :| : |:    :||: |:|||:   : :: ||:
Db          1 MCQSRYLLFLATLAL---LNHLSLARVIPVSGPA----RCLSQSRNLLKTTDDMVKTARE 53

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLIT 109
                |: ||||:|:|||||||:|:|||:: ||||||  ||||||:|| |  |
Db         54 KLKHYSCTAEDIDHEDITRDQTSTLKTCLPLELHKNESCLATRETSSTT 102


RESULT 10
Q9NXJ6
ID   Q9NXJ6      PRELIMINARY;      PRT;   444 AA.
AC   Q9NXJ6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CDNA FLJ20207 fis, clone COLF1609.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON MUCOSA;
RA   Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA   Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
RA   Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK000214; BAA91014.1; -.
DR   InterPro; IPR000583; GATase_2.
DR   InterPro; IPR004129; GDPD.
DR   Pfam; PF03009; GDPD; 1.
DR   PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
SQ   SEQUENCE   444 AA;  50585 MW;  52AF60FF1F76B6E5 CRC64;

  Query Match             8.7%;  Score 98.5;  DB 4;  Length 444;
  Best Local Similarity   21.9%;  Pred. No. 0.67;
  Matches   59;  Conservative   36;  Mismatches   95;  Indels   79;  Gaps   12;

Qy          4 PRGLLLVTI--LVLLSHLDHLTWA-------RSLPTASPSPGIFQCLNHSQNLLRAVSNT 54
              |: |||:    :||: :|  |  :        | ||   | ||:   : |    : |  ||
Db        187 PKILLLLLFFGVVLVIYLAPLCISSPCIMEPRDLP---PKPGL---VGHRGAPMLAPENT 240

Qy         55 LQKARQTLELYSCTSEEID-----------HEDITKDKTSTVEACLPLELTMNESCLASR 103
              |   |:| |    |  | |           |    :|: | :  |  :| : |  :
Db        241 LMSLRKTAEC-GATVFETDVMVSSDGVPFLMHDEHLSRTTNVASVFPTRITAHSSDFSWT 299

Qy        104 EISLITNGSCLASGK--------------ASFMTVLCLSSIYEDLKMYQMEFKAMNAKL 148
              |:  :  ||     :              |   ||  |  : |       |  |:|  :
Db        300 ELKRLNAGSWFLERRPFWGAKPLAGPDQKEAESQTVPALEELLE-------EAAALNLSI 352

Qy        149 LMD----PKRQIFLDQNMLTAIDELL-----QALNF-----------------NSVTVP 181
              : |    |:   : |  ::  :: :|     ||: |                   : |
Db        353 MFDLRRPPQNHTYYDTFVIQTLETVLNARVPQAMVFWLPDEDRAMSNDGHLECARYMDVR 412

Qy        182 QKSSLEEPDFYKTKIKLC---ILLHAFRI 207
              : :    | |  : ||:|   |  |  ||
Db        413 EATERGGPSFLTSPIKICHYWISRHCIRI 441


RESULT 11
Q9SJT3
ID   Q9SJT3      PRELIMINARY;      PRT;   816 AA.
AC   Q9SJT3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   At2g21450 protein.
GN   AT2G21450.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
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RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA   Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA   Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA   Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA   Salzberg S.L., Fraser C.M., Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Lin X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC006841; AAD23689.1; -.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR000330; SNF2_N.
DR   Pfam; PF00271; helicase_C; 1.
DR   Pfam; PF00176; SNF2_N; 2.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
KW   ATP-binding; Helicase.
SQ   SEQUENCE   816 AA;  93297 MW;  A5B249A1C2FF7A9C CRC64;

  Query Match             8.6%;  Score 97.5;  DB 10;  Length 816;
  Best Local Similarity   23.2%;  Pred. No. 1.7;
  Matches   52;  Conservative   34;  Mismatches   79;  Indels   59;  Gaps    9;

Qy         45 QNLLRAVSNTLQKARQ-------TLELYS--CTSEEIDHEDITKDKTSTVEACL--PLEL 93
              ||  :  | | |   |        | |: |   :  ||          :|::|      :||
Db        442 QNNVEEVFNILDLVRPKFLKRPGTREIVSRIMSKAEIPRGKQVNQSSSSIEGTFFAAVEL 501

Qy         94 TMNESCLASREISLI---------------TNGSCLASGKASFMTVLCLSSIYED----- 133
              |:  |  | : |||                : | |  | : |  :| ||||  |
Db        502 TLQRSTNFSAKASLIKDLREMTRNILHYHKADFSGLLPGLSEFTVMLNLSSIQRDEVKGL 561

Qy        134 LKMYQMEFKAMNAKLLMDPKRQIFLDQN-------------MLTAIDELLQALNFNSVTV 180
              ||   :  :: | | : || : ||::|              :  :|::|: :|     |
Db        562 RKMELFKQISLGAALYIHPKLKSFLEENPSNGEKGFSDNNTTVMKLDKMLKKINVRD-GV 620

Qy        181 PQKSSLEEPDFYKTKIKLC-------ILLHAFRIRAVTIDRMMS 217
              |       |:   : ||       ::   : :   |::|:||
Db        621 KMK-------FFLNLLALCESTGEKLLVFSQYIVPIKTLERLMS 657


RESULT 12
Q92GE9
ID   Q92GE9      PRELIMINARY;      PRT;  1583 AA.
AC   Q92GE9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical protein RC1174.
GN   RC1174.
OS   Rickettsia conorii.
OC   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia.
OX   NCBI_TaxID=781;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MALISH 7;
RX   MEDLINE=21442074; PubMed=11557893;
RA   Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA   Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA   Raoult D.;
RT   "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL   Science 293:2093-2098(2001).
DR   EMBL; AE008665; AAL03712.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   1583 AA;  181365 MW;  FB3FE733C2872625 CRC64;

  Query Match             8.2%;  Score 93;  DB 16;  Length 1583;
  Best Local Similarity   22.6%;  Pred. No. 9.8;
  Matches   47;  Conservative   40;  Mismatches   71;  Indels   50;  Gaps    9;

Qy         34 SPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLEL 93
              | |:  | :|  |:  |:|: :   : |||          :   :  | |  ||     ||
Db       1140 SAGV-DCSDHEVNIKIALSSAITSGKITLE---------ERNKLLNDMTKQVE-----EL 1184

Qy         94 TMNESCLASREISLITNGSCLASGKASFMTVLCLS---SIYEDLKMYQME---------- 140
                : ::   :  |:::     |         ||  ||    | |: |: : |
Db       1185 VLIDNYKQTEAITIMQLSPTL--------TVNILSQFIDILEEEKVLERENEFLPSAEEL 1236

Qy        141 -FKAMNAKLLMDPKRQIFLDQNMLTAIDELLQAL-----NFNSVTVPQKSSLEEPDFYKT 194
               :||: ::|  |:  | |  :  :|  ||: :       |::  :        |:  :
Db       1237 NSRAMSGEVLTRPELCILLSYSKRSAYHELINSTFSHDKYFDAYLIDY-----FPEMMQK 1291

Qy        195 KIKLCILLHAFR---IRAVTIDRMMSYL 219
              | :  || |  :   |: |||:::|: |
Db       1292 KFRNEILSHPLKHEIIKTVTINKIMNQL 1319


RESULT 13
Q9HCC8
ID   Q9HCC8      PRELIMINARY;      PRT;  539 AA.
AC   Q9HCC8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Osteoblast differentiation promoting factor.
GN   HOBDPF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imai Y.;
RT   "Human cDNA related with osteoblast differentiation.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB048363; BAB13350.1; -.
DR   InterPro; IPR000583; GATase_2.
DR   InterPro; IPR004129; GDPD.
DR   Pfam; PF03009; GDPD; 1.
DR   PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
SQ   SEQUENCE   539 AA;  61728 MW;  8271C3A74766D540 CRC64;

  Query Match             8.2%;  Score 92.5;  DB 4;  Length 539;
  Best Local Similarity   23.0%;  Pred. No. 3;
  Matches   52;  Conservative   30;  Mismatches   85;  Indels   59;  Gaps   10;

Qy          4 PRGLLLVTI--LVLLSHLDHLTWA-------RSLPTASPSPGIFQCLNHSQNLLRAVSNT 54
              |: |||:    :||: :|  |  :        | ||   | ||:   : |    : |  ||
Db        187 PKILLLLLFFGVVLVIYLAPLCISSPCIMEPRDLP---PKPGL---VGHRGAPMLAPENT 240

Qy         55 LQKARQTLELYSCTSEEID-----------HEDITKDKTSTVEACLPLELTMNESCLASR 103
              |   |:| |     |  | |              |     :|: | :  |  :| : |  :
Db        241 LMSLRKTAEC-GATVFETDVMVSSDGVPFLMHDEHLSRTTNVASVFPTRITAHSSDFSWT 299

Qy        104 EISLITNGSCLASGK--------------ASFMTVLCLSSIYEDLKMYQMEFKAMNAKL 148
              |:  :  ||     :              |   ||  |  : |       |  |:|  :
Db        300 ELKRLNAGSWFLERRPFWGAKPLAGPDQKEAESQTVPALEELLE-------EAAALNLSI 352

Qy        149 LMD----PKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPD 190
              : |    |:   : |  ::  :: :| |       |||      ||
Db        353 MFDLRRPPQNHTYYDTFVIQTLETVLNA------RVPQAMVFWLPD 392


RESULT 14
Q9VZU0
ID   Q9VZU0      PRELIMINARY;      PRT;  537 AA.
AC   Q9VZU0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
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DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CG12032 protein.
GN   CG12032.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003477; AAF47727.1; -.
DR   FlyBase; FBgn0035408; CG12032.
DR   InterPro; IPR000051; SAM_bind.
DR   InterPro; IPR003402; Unk_Met10.
DR   Pfam; PF02475; Met_10; 1.
SQ   SEQUENCE   537 AA;  61413 MW;  686BC8CBBBCC70D4 CRC64;

  Query Match             8.0%;  Score 90;  DB 5;  Length 537;
  Best Local Similarity   25.1%;  Pred. No. 5.2;
  Matches   47;  Conservative   29;  Mismatches   75;  Indels   36;  Gaps   11;

Qy         27 SLPTASP---------SPGIFQCLNHSQNLLRAVSN---TLQKARQTLELYSCTSEEIDH 74
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Db        241 SIPAAKKRCHVLANDLNPESFRWLQHNAKRNKCLPNIKMSNKDGRQFI------VEEL-R 293

Qy         75 EDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDL 134
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Db        294 EDLLKRLCTTDTTTYGIHITMNLPAMAVEFLDAF-RGLYSADELAQLPTNVC----YPTV 348

Qy        135 KMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDE-LLQALNFNSVTVPQKSSLEEPDFYK 193
               :|    |  | | |:   ||: :: |:  ::|| ||| :||     | |      | |:
Db        349 HVYSFA-KGENTKELV---RQL-VESNLGASLDENLLQGINFVRNVAPNK------DMYR 397

Qy        194 TKIKLCI 200
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Db        398 VSFKLSL 404


RESULT 15
O04143
ID   O04143      PRELIMINARY;      PRT;   581 AA.
AC   O04143;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 63.5 kDa protein.
OS   Silene latifolia (White campion).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX   NCBI_TaxID=37657;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FLOWERBUDS;
RX   MEDLINE=98042964; PubMed=9375394;
RA   Barbacar N., Hinnisdaels S., Farbos I., Moneger F., Lardon A.,
RA   Delichere C., Mouras A., Negrutiu I.;
RT   "Isolation of early genes expressed in reproductive organs of the
RT   dioecious white campion (Silene latifolia) by subtraction cloning
RT   using an asexual mutant.";
RL   Plant J. 12:805-817(1997).
DR   EMBL; Y12529; CAA73132.1; -.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR003592; LRR_out.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00560; LRR; 17.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00370; LRR; 5.
DR   SMART; SM00369; LRR_TYP; 4.
KW   Hypothetical protein.
SQ   SEQUENCE   581 AA;  63516 MW;  52E2D16AD1AA3642 CRC64;

  Query Match             8.0%;  Score 90;  DB 10;  Length 581;
  Best Local Similarity   21.7%;  Pred. No. 5.7;
  Matches   59;  Conservative   42;  Mismatches   75;  Indels   96;  Gaps   13;

Qy         29 PTAS---------PSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYS----------CTS 69
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Db        321 PTAALLKYLRGRLPSAEEAQVMTPSKDNMVAMASRLSITTKELSLVGMGLIAVPPEVCES 380

Qy         70 EEIDHEDITKDKTS----TVEACLPLELTM-----------------NESCL------- 100
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Db        381 NEITKVDLSKNSIQELPVTLSACSSLEVLILSRNKIKDWPEDALKSLPNLTCLRLDNNPL 440

Qy        101 ---------ASREISLITNGSCLAS--GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLL 149
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Db        441 NKVPLNGFDAVPRLQILDLSGCVSSLVDNPAFASLQHLVELY----LRRVKLQEVPSDIL 496

Qy        150 MDPKRQIF-LDQNMLTAIDELLQ--------ALNFNSV-TVPQKSSLEEPDFYKTKIKLC 199
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Db        497 MLRKLQILDLSQNSLHSIPQGFQNLTSLTELDLSDNSIGTLPPELGLLEPS--------- 547

Qy        200 ILLHAFR--------IRAVTIDR----MMSYL 219
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Search completed: July 15, 2003, 11:06:06
Job time : 22.6722 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 10:59:19 ; Search time 7.61505 Seconds
(without alignments)
857.760 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	940.5	83.4	219	1	US-08-186-529-4	Sequence 4, Appli
2	940.5	83.4	219	1	US-08-640-386A-4	Sequence 4, Appli
3	940.5	83.4	253	1	US-08-265-087-4	Sequence 4, Appli
4	940.5	83.4	253	1	US-08-621-493-4	Sequence 4, Appli
5	940.5	83.4	253	2	US-08-684-687-4	Sequence 4, Appli
6	940.5	83.4	253	2	US-08-965-688-4	Sequence 4, Appli
7	940.5	83.4	253	4	US-09-260-173-4	Sequence 4, Appli
8	934.5	82.8	219	2	US-08-751-767A-2	Sequence 2, Appli
9	869	77.0	519	2	US-08-751-767A-12	Sequence 12, Appl
10	869	77.0	540	2	US-08-751-767A-8	Sequence 8, Appli
11	869	77.0	540	2	US-08-751-767A-10	Sequence 10, Appl
12	591.5	52.4	215	2	US-08-659-206A-2	Sequence 2, Appli
13	591.5	52.4	215	2	US-08-659-206A-5	Sequence 5, Appli
14	579.5	51.4	215	2	US-08-385-335A-12	Sequence 12, Appl
15	84.5	7.5	2482	1	US-08-328-254-6	Sequence 6, Appli
16	84.5	7.5	2511	4	US-09-261-907-2	Sequence 2, Appli
17	83.5	7.4	132	2	US-08-649-991-64	Sequence 64, Appl
18	83.5	7.4	3248	1	US-08-353-700-1	Sequence 1, Appli
19	83.5	7.4	3248	5	PCT-US95-16216-1	Sequence 1, Appli
20	82.5	7.3	2509	1	US-08-469-005A-10	Sequence 10, Appl
21	80	7.1	138	2	US-08-649-991-84	Sequence 84, Appl
22	79.5	7.0	132	2	US-08-649-991-105	Sequence 105, App
23	79.5	7.0	132	2	US-08-649-991-106	Sequence 106, App
24	79.5	7.0	132	2	US-08-649-991-112	Sequence 112, App
25	78.5	7.0	132	2	US-08-649-991-97	Sequence 97, Appl
26	78.5	7.0	132	2	US-08-649-991-98	Sequence 98, Appl
27	78.5	7.0	132	2	US-08-649-991-113	Sequence 113, App
28	78.5	7.0	1091	3	US-08-986-485-5	Sequence 5, Appli
29	78	6.9	1786	2	US-08-477-451-16	Sequence 16, Appl
30	77.5	6.9	143	2	US-08-477-451-37	Sequence 37, Appl
31	76.5	6.8	132	2	US-08-649-991-86	Sequence 86, Appl
32	76.5	6.8	132	2	US-08-649-991-87	Sequence 87, Appl
33	76.5	6.8	132	2	US-08-649-991-95	Sequence 95, Appl
34	76.5	6.8	135	2	US-08-649-991-79	Sequence 79, Appl
35	76	6.7	133	2	US-08-649-991-72	Sequence 72, Appl
36	75.5	6.7	132	2	US-08-649-991-70	Sequence 70, Appl
37	75.5	6.7	226	4	US-09-134-001C-3578	Sequence 3578, Ap
38	75.5	6.7	500	1	US-08-375-510-1	Sequence 1, Appli
39	75.5	6.7	500	2	US-08-487-657-1	Sequence 1, Appli
40	75.5	6.7	500	4	US-09-309-572-16	Sequence 16, Appl
41	74.5	6.6	132	2	US-08-649-991-81	Sequence 81, Appl
42	74.5	6.6	132	2	US-08-649-991-93	Sequence 93, Appl
43	74.5	6.6	132	2	US-08-649-991-108	Sequence 108, App
44	74.5	6.6	132	2	US-08-649-991-111	Sequence 111, App
45	74.5	6.6	136	2	US-08-649-991-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-08-186-529-4
; Sequence 4, Application US/08186529
; Patent No. 5573764
; GENERAL INFORMATION:
; APPLICANT: Sykes, Megan
; APPLICANT: Wolf, Stanley F.
; TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
; TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc., Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,529
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: GI 5225
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8401
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-186-529-4

Query Match 83.4%; Score 940.5; DB 1; Length 219;
Best Local Similarity 84.2%; Pred. No. 1.2e-97;
Matches 187; Conservative 9; Mismatches 23; Indels 3; Gaps 1;

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Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
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Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
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Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 219


RESULT 2
US-08-640-386A-4
; Sequence 4, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-640-386A-4

  Query Match             83.4%;  Score 940.5;  DB 1;  Length 219;
  Best Local Similarity   84.2%;  Pred. No. 1.2e-97;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

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Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 219


RESULT 3
US-08-265-087-4
; Sequence 4, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  253 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-265-087-4

  Query Match             83.4%;  Score 940.5;  DB 1;  Length 253;
  Best Local Similarity   84.2%;  Pred. No. 1.5e-97;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | |||| ||| |||| |:|| |:| ||:| ||:|||||||||||| ||||||
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RESULT 4
US-08-621-493-4
; Sequence 4, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
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;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  253 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-621-493-4

  Query Match             83.4%;  Score 940.5;  DB 1;  Length 253;
  Best Local Similarity   84.2%;  Pred. No. 1.5e-97;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:||||||||||| ||||||
Db         35 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 91

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
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Db         92 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 151

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
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Db        152 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 211

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
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Db        212 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 253


RESULT 5
US-08-684-687-4
; Sequence 4, Application US/08684687
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  253 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-684-687-4

  Query Match             83.4%;  Score 940.5;  DB 2;  Length 253;
  Best Local Similarity   84.2%;  Pred. No. 1.5e-97;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:||||||||||| ||||||
Db         35 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 91

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | ||||||||||||||||||||||||||||| ||||| ||| | ||||||||| | |
Db         92 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 151

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  |||||||||||||:||| ||||||||||||||||||||  ||||:||||||| ||
Db        152 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 211

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||||||||:|||||:|
Db        212 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 253


RESULT 6
US-08-965-688-4
; Sequence 4, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/965,688
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/621,493
;       FILING DATE:  25-MAR-1996
;       APPLICATION NUMBER:  08/265,087
;       FILING DATE:  17-JUN-1994
;       APPLICATION NUMBER:  US 08/229,282
;       FILING DATE:  18-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST51AUSA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9206
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  253 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-965-688-4

  Query Match             83.4%;  Score 940.5;  DB 2;  Length 253;
  Best Local Similarity   84.2%;  Pred. No. 1.5e-97;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||||| ||||||
Db         35 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 91

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | ||||||||||||||||||||||||||| ||||| ||| | |||||||||| | |
Db         92 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 151

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  |||||||||||||:||| ||||||||||||||||||  ||||:||||||| ||
Db        152 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 211

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||:|||||:|
Db        212 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 253


RESULT 7
US-09-260-173-4
; Sequence 4, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 253 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-260-173-4

  Query Match             83.4%;  Score 940.5;  DB 4;  Length 253;
  Best Local Similarity   84.2%;  Pred. No. 1.5e-97;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||||| ||||||
Db         35 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 91

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | ||||||||||||||||||||||||||| ||||| ||| | |||||||||| | |
Db         92 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 151

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  |||||||||||||:||| ||||||||||||||||||  ||||:||||||| ||
Db        152 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 211

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||:|||||:|
Db        212 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 253


RESULT 8
US-08-751-767A-2
; Sequence 2, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-2

  Query Match             82.8%;  Score 934.5;  DB 2;  Length 219;
  Best Local Similarity   83.8%;  Pred. No. 5.5e-97;
  Matches  186;  Conservative    9;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:||||||||||| ||||||
Db          1 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | ||||||||||||||||||||||||||||| ||||| ||| | |||||||| | |
Db         58 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  |||||||||||||:||| ||||||||||||||||||  ||||:|||||| ||
Db        118 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||||: ||||:|
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 219


RESULT 9
US-08-751-767A-12
; Sequence 12, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  519 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-12

  Query Match             77.0%;  Score 869;  DB 2;  Length 519;
  Best Local Similarity   85.9%;  Pred. No. 4.9e-89;
  Matches  170;  Conservative    9;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 84
              :|:|| |:| ||:| ||:|||||||||||| ||||||||| | ||||||||||||||||||
Db        322 SRNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 381

Qy         85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144
              |||||||||| ||||| ||| | ||||||||| | |||  |||||||||||||:||| |
Db        382 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 441

Qy        145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204
              ||||||||||||||||||  ||||:|||||| ||||||||||||||||||||||||||||
Db        442 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 501

Qy        205 FRIRAVTIDRMMSYLNSS 222
              ||||||||||: ||||:|
Db        502 FRIRAVTIDRVTSYLNAS 519


RESULT 10
US-08-751-767A-8
; Sequence 8, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-8

  Query Match             77.0%;  Score 869;  DB 2;  Length 540;
  Best Local Similarity   85.9%;  Pred. No. 5.2e-89;
  Matches  170;  Conservative    9;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 84
              :|:|| |:| ||:| ||:|||||||||||| ||||||||| | ||||||||||||||||||
Db        343 SRNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 402
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Qy          85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144
               |||||||||| ||||| ||| | |||||||| | ||| |||||||||||||:||| |
Db         403 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 462

Qy         145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204
               |||||||||||||||||  ||||:||||||| |||||||||||||||||||||||||||
Db         463 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 522

Qy         205 FRIRAVTIDRMMSYLNSS 222
               |||||||||| |||| |
Db         523 FRIRAVTIDRVTSYLNAS 540


RESULT 11
US-08-751-767A-10
; Sequence 10, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-10

  Query Match             77.0%;  Score 869;  DB 2;  Length 540;
  Best Local Similarity   85.9%;  Pred. No. 5.2e-89;
  Matches  170;  Conservative    9;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 84
               :|:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db         343 SRNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 402

Qy          85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144
               |||||||||| ||||| ||| | |||||||| | ||| |||||||||||||:||| |
Db         403 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 462

Qy         145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204
               |||||||||||||||||  ||||:||||||| |||||||||||||||||||||||||||
Db         463 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 522

Qy         205 FRIRAVTIDRMMSYLNSS 222
               |||||||||| |||| |
Db         523 FRIRAVTIDRVTSYLNAS 540


RESULT 12
US-08-659-206A-2
; Sequence 2, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH:  215 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-2

  Query Match             52.4%;  Score 591.5;  DB 2;  Length 215;
  Best Local Similarity   54.5%;  Pred. No. 1.9e-58;
  Matches  121;  Conservative   36;  Mismatches   58;  Indels    7;  Gaps    2;

Qy           1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
               ||  | || :  | |   |:||: || :| : |:    :||: |:|||:   : :: ||:
Db           1 MCQSRYLLFLATLAL---LNHLSLARVIPVSGPA----RCLSQSRNLLKTTDDMVKTARE 53

Qy          61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
               |: ||||:|:|||||||:|:|||:: |||||  ||||||:|| |  | ||||   | |
Db          54 KLKHYSCTAEDIDHEDITRDQTSTLKTCLPLELHKNESCLATRETSSTTRGSCLPPQKTS 113

Qy         121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               |  ||| |||||||||| ||:|:|| |     :|| ||: || |||||:|:|| |  |:
Db         114 LMMTLCLGSIYEDLKMYQTEFQAINAALQNHNHQQIILDKGMLVAIDELMQSLNHNGETL 173

Qy         181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               ||  :.| | |: |:|||||||||  | |||:|:| ||:|:
Db         174 RQKPPVGEADPYRVKMKLCILLHAFSTRVVTINRVMGYLSSA 215


RESULT 13
US-08-659-206A-5
; Sequence 5, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
```

```
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 215 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-5

  Query Match             52.4%;  Score 591.5;  DB 2;  Length 215;
  Best Local Similarity   54.5%;  Pred. No. 1.9e-58;
  Matches  121;  Conservative   36;  Mismatches   58;  Indels    7;  Gaps    2;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
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Db          1 MCQSRYLLFLATLAL---LNHLSLARVIPVSGPA----RCLSQSRNLLKTTDDMVKTARE 53

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
               |: ||||:|:|||||||:|:|||:: |||||  ||||||:|| |  | ||||   | |
Db         54 KLKHYSCTAEDIDHEDITRDQTSTLKTCLPLELHKNESCLATRETSSTTRGSCLPPQKTS 113

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
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Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
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Db        174 RQKPPVGEADPYRVKMKLCILLHAFSTRVVTINRVMGYLSSA 215


RESULT 14
US-08-385-335A-12
; Sequence 12, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  215 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-385-335A-12

  Query Match             51.4%;  Score 579.5;  DB 2;  Length 215;
  Best Local Similarity   54.6%;  Pred. No. 4.2e-57;
  Matches  119;  Conservative   36;  Mismatches   56;  Indels    7;  Gaps    2;

Qy          5 RGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLEL 64
              | || :  | |   |:||: || :| : |:    :||: |:|||:   : :: ||: |:
Db          5 RYLLFLATLAL---LNHLSLARVIPVSGPA----RCLSQSRNLLKTTDDMVKTAREKLKH 57

Qy         65 YSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTV 124
              ||||:|:|||||||:|:|||:: |||||  ||||||:|| |  | ||||   | | |
Db         58 YSCTAEDIDHEDITRDQTSTLKTCLPLELHKNESCLATRETSSTTRGSCLPPQKTSLMMT 117

Qy        125 LCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKS 184
              ||| |||||||||| ||:|:|| |     :|| ||: || |||||:|:|| |  |: ||
Db        118 LCLGSIYEDLKMYQTEFQAINAALQNHNHQQIILDKGMLVAIDELMQSLNHNGETLRQKP 177

Qy        185 SLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              : | | |: |:|||||||||  | |||:|:| ||:|:
Db        178 PVGEADPYRVKMKLCILLHAFSTRVVTINRVMGYLSSA 215


RESULT 15
US-08-328-254-6
; Sequence 6, Application US/08328254
; Patent No. 5710022
;  GENERAL INFORMATION:
;    APPLICANT:  Zhu, Xueliang
;    APPLICANT:  Lee, Wen-Hwa
;    TITLE OF INVENTION:  A No. 5710022el Nuclear Mitotic Phosphoprotein
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,254
;      FILING DATE:  24-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,239
;      FILING DATE:  22-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1191
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
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;       TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2482 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-328-254-6

  Query Match             7.5%;  Score 84.5;  DB 1;  Length 2482;
  Best Local Similarity   20.7%;  Pred. No. 7.9;
  Matches   39;  Conservative   43;  Mismatches   77;  Indels   29;  Gaps    7;

Qy         43 HSQNLLRAVSNTLQKARQTLELYSCTSEEIDHE--DITKDKTSTVEACLPLELTMNESCL 100
              | |  |:    :|:|  | | |  |   |::::   : |:|   |:    |:  ::||
Db       1400 HLQEKLQ----SLEKDSQALSLTKC---ELENQIAQLNKEKELLVKESESLQARLSESDY 1452

Qy        101 ASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFL-- 158
                :|     : :  |: :    | |||  |::   :   : :  ::  | |:|: :
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Qy        159 --------DQNMLTAIDELLQAL-----NFNSVTVPQKSSLEEPDFYKTKI-KLCILLHA 204
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Db       1509 KLKERERENDSLKDKVENLERELQMSEENQELVILDAENSKAEVETLKTQIEEMARSLKV 1568

Qy        205 FRIRAVTI 212
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Db       1569 FELDLVTL 1576


Search completed: July 15, 2003, 11:09:58
Job time : 9.61506 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 11:03:04 ; Search time 10.3649 Seconds
(without alignments)
2493.521 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1128	100.0	222	10	US-09-917-265-47	Sequence 47, Appl
2	1128	100.0	222	10	US-09-917-265-105	Sequence 105, App
3	1046	92.7	222	12	US-10-079-616-3	Sequence 3, Appli
4	1043	92.5	222	10	US-09-917-265-33	Sequence 33, Appl
5	994	88.1	197	10	US-09-917-265-50	Sequence 50, Appl
6	970	86.0	511	10	US-09-917-265-67	Sequence 67, Appl
7	970	86.0	533	10	US-09-917-265-62	Sequence 62, Appl
8	940.5	83.4	253	10	US-09-924-703-6	Sequence 6, Appli
9	934.5	82.8	219	9	US-10-172-399-6	Sequence 6, Appli
10	934.5	82.8	219	10	US-09-754-014-5	Sequence 5, Appli
11	934.5	82.8	219	10	US-09-836-866-3	Sequence 3, Appli
12	932	82.6	197	12	US-10-079-616-4	Sequence 4, Appli
13	930	82.4	511	10	US-09-917-265-44	Sequence 44, Appl
14	930	82.4	533	10	US-09-917-265-39	Sequence 39, Appl
15	929	82.4	197	10	US-09-917-265-36	Sequence 36, Appl
16	889	78.8	187	10	US-09-917-265-102	Sequence 102, App
17	876.5	77.7	527	10	US-09-828-825-2	Sequence 2, Appli
18	875.5	77.6	537	10	US-09-828-825-8	Sequence 8, Appli
19	875.5	77.6	537	10	US-09-828-825-16	Sequence 16, Appl
20	875.5	77.6	542	10	US-09-828-825-6	Sequence 6, Appli
21	875.5	77.6	542	10	US-09-828-825-14	Sequence 14, Appl
22	875.5	77.6	547	10	US-09-828-825-10	Sequence 10, Appl
23	875.5	77.6	547	10	US-09-828-825-12	Sequence 12, Appl
24	875	77.6	503	9	US-09-920-262A-9	Sequence 9, Appli
25	872.5	77.3	526	10	US-09-828-825-4	Sequence 4, Appli
26	591.5	52.4	215	9	US-10-172-399-2	Sequence 2, Appli
27	109	9.7	21	12	US-10-079-616-20	Sequence 20, Appl
28	92.5	8.2	539	9	US-10-028-072-140	Sequence 140, App
29	92.5	8.2	539	9	US-10-121-049-140	Sequence 140, App
30	92.5	8.2	539	9	US-10-123-904-140	Sequence 140, App
31	92.5	8.2	539	9	US-10-140-470-140	Sequence 140, App
32	92.5	8.2	539	9	US-10-175-746-140	Sequence 140, App
33	92.5	8.2	539	9	US-10-176-918-140	Sequence 140, App
34	92.5	8.2	539	9	US-10-176-921-140	Sequence 140, App
35	92.5	8.2	539	9	US-10-137-865-140	Sequence 140, App
36	92.5	8.2	539	9	US-10-140-474-140	Sequence 140, App
37	92.5	8.2	539	9	US-10-142-431-140	Sequence 140, App
38	92.5	8.2	539	9	US-10-143-114-140	Sequence 140, App
39	92.5	8.2	539	9	US-10-140-002-140	Sequence 140, App
40	92.5	8.2	539	9	US-10-142-419-140	Sequence 140, App
41	92.5	8.2	539	9	US-10-152-031-4	Sequence 4, Appli
42	92.5	8.2	539	9	US-10-123-262-140	Sequence 140, App
43	92.5	8.2	539	9	US-10-142-423-140	Sequence 140, App
44	92.5	8.2	539	9	US-10-121-050-140	Sequence 140, App
45	92.5	8.2	539	9	US-10-141-755-140	Sequence 140, App

ALIGNMENTS

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RESULT 1
US-09-917-265-47
; Sequence 47, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 222
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-47

  Query Match            100.0%;  Score 1128;  DB 10;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-103;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
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Db          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
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Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
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Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
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RESULT 2
US-09-917-265-105
; Sequence 105, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
;   LENGTH: 222
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-105

  Query Match            100.0%;  Score 1128;  DB 10;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 6.5e-103;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
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Db         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
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Db        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222


RESULT 3
US-10-079-616-3
; Sequence 3, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 222 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-079-616-3

  Query Match            92.7%;  Score 1046;  DB 12;  Length 222;
  Best Local Similarity  92.3%;  Pred. No. 7.4e-95;
  Matches  205;  Conservative    8;  Mismatches    9;  Indels    0;  Gaps    0;

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Db          1 MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
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Db         61 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASRKTS 120

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
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Db        121 FMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTV 180

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
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Db        181 PQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 222


RESULT 4
US-09-917-265-33
; Sequence 33, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 222
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-33

  Query Match            92.5%;  Score 1043;  DB 10;  Length 222;
  Best Local Similarity  91.9%;  Pred. No. 1.5e-94;
  Matches  204;  Conservative    9;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              |||||||||||||||:|||||: ||:||| :||||:|||||||| ||||:|||||||||
Db          1 MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQ 60

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||| | |
```

```
Db          61 TLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASRKTS 120

Qy         121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
               ||| |||||||||||||||:|||||||||||||||||||||||||||||||| |||||
Db         121 FMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTV 180

Qy         181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
               || |||||||||||||||||||||||||||||:|||||||:|
Db         181 PQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNAS 222


RESULT 5
US-09-917-265-50
; Sequence 50, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-50

  Query Match             88.1%;  Score 994;  DB 10;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 8e-90;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60

Qy          86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120

Qy         146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180

Qy         206 RIRAVTIDRMMSYLNSS 222
               |||||||||||||||||
Db         181 RIRAVTIDRMMSYLNSS 197


RESULT 6
US-09-917-265-67
; Sequence 67, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-67

  Query Match             86.0%;  Score 970;  DB 10;  Length 511;
  Best Local Similarity   96.5%;  Pred. No. 6.9e-87;
  Matches  191;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 84
               :|:||| :||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db         314 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 373

Qy          85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144
               ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db         374 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 433

Qy         145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         434 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 493

Qy         205 FRIRAVTIDRMMSYLNSS 222
               ||||||||:||||||||
Db         494 FRIRAVTINRMMSYLNSS 511


RESULT 7
US-09-917-265-62
; Sequence 62, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-62

  Query Match             86.0%;  Score 970;  DB 10;  Length 533;
  Best Local Similarity   96.5%;  Pred. No. 7.3e-87;
  Matches  191;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 84
               :|:||| :||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db         336 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 395

Qy          85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         396 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 455

Qy         145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         456 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 515

Qy         205 FRIRAVTIDRMMSYLNSS 222
               ||||||||:||||||||
Db         516 FRIRAVTINRMMSYLNSS 533


RESULT 8
US-09-924-703-6
; Sequence 6, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
```

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;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic amino
;   OTHER INFORMATION: acid sequence of the 30 kD subunit of NKSF
US-09-924-703-6

  Query Match             83.4%;  Score 940.5;  DB 10;  Length 253;
  Best Local Similarity   84.2%;  Pred. No. 2e-84;
  Matches  187;  Conservative    9;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||||| ||||||
Db         35 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 91

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | ||||||||||||||||||||||||||||| ||||| ||| | |||||||| | |
Db         92 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 151

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  ||||||||||||||:||| |||||||||||||||||  ||||:||||||| ||
Db        152 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 211

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||||||:|||||:|
Db        212 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 253


RESULT 9
US-10-172-399-6
; Sequence 6, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-172-399-6

  Query Match             82.8%;  Score 934.5;  DB 9;  Length 219;
  Best Local Similarity   83.8%;  Pred. No. 6.5e-84;
  Matches  186;  Conservative    9;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||||| ||||||
Db          1 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | ||||||||||||||||||||||||||||| ||||| ||| | |||||||| | |
Db         58 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  ||||||||||||||:||| |||||||||||||||||  ||||:||||||| ||
Db        118 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||||||:|||||:|
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 219


RESULT 10
US-09-754-014-5
; Sequence 5, Application US/09754014
; Patent No. US20020119940A1
;  GENERAL INFORMATION:
;       APPLICANT: Jeff No. US20020119940A1dstrom
;                  Bruce Freimark
;                  Deepa Deshpande
;       TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                           AND USES
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lyon & Lyon
;            STREET: 633 West Fifth Street
;                    Suite 4700
;            CITY: Los Angeles
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 90071-2066
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                         storage
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: IBM P.C. DOS 5.0
;            SOFTWARE: FastSEQ for Windows 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/754,014
;            FILING DATE: 03-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/948,958
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Berkman, Charles S.
;            REGISTRATION NUMBER: 38,077
;            REFERENCE/DOCKET NUMBER: 226/284
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (213) 489-1600
;            TELEFAX: (213) 955-0440
;            TELEX: 67-3510
;  INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 219 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-754-014-5

  Query Match             82.8%;  Score 934.5;  DB 10;  Length 219;
  Best Local Similarity   83.8%;  Pred. No. 6.5e-84;
  Matches  186;  Conservative    9;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||||| ||||||
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Db          1 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | |||||||||||||||||||||||||||| ||||| ||| | |||||||| | |
Db         58 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  |||||||||||||:||| |||||||||||||||||||  ||||:||||||| ||
Db        118 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||: ||||:|
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 219


RESULT 11
US-09-836-866-3
; Sequence 3, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020123473A1dstrom, Jeff
;                   Freimark, Bruce
;                   Deshpande, Deepa
;        TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                            DELIVERY SYTEMS AND USES
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/836,866
;             FILING DATE: 16-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/949,160
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 226/285
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 219 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-836-866-3

  Query Match           82.8%;  Score 934.5;  DB 10;  Length 219;
  Best Local Similarity  83.8%;  Pred. No. 6.5e-84;
  Matches  186;  Conservative    9;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQ 60
              ||| | ||||  |||   ||||: ||:|| |:| ||:| ||:|||||||||||| ||||||
Db          1 MCPARSLLLVATLVL---LDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQ 57

Qy         61 TLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKAS 120
              ||| | |||||||||||||||||||||||||||| ||||| ||| | |||||||| | |
Db         58 TLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTS 117

Qy        121 FMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTV 180
              ||  |||||||||||||:||| |||||||||||||||||||  ||||:||||||| ||
Db        118 FMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETV 177

Qy        181 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS 222
              ||||||||||||||||||||||||||||||: ||||:|
Db        178 PQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 219


RESULT 12
US-10-079-616-4
; Sequence 4, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 197 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-079-616-4

  Query Match           82.6%;  Score 932;  DB 12;  Length 197;
  Best Local Similarity  92.9%;  Pred. No. 9.9e-84;
  Matches  183;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85
              |:||| :||||:||||||| ||||:|||||||||||| ||||||||||||||||||||
Db          1 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 60

Qy         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145
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                ||||||||||||||||||||||||||||||| | |||| ||||||||||||||:||||||
Db          61 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 120

Qy         146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205
               ||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Db         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 180

Qy         206 RIRAVTIDRMMSYLNSS 222
               |||||||:|||||||||
Db         181 RIRAVTINRMMSYLNSS 197


RESULT 13
US-09-917-265-44
; Sequence 44, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-44

  Query Match             82.4%;  Score 930;  DB 10;  Length 511;
  Best Local Similarity   91.9%;  Pred. No. 5.8e-83;
  Matches  182;  Conservative    8;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 84
               :|:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db         314 SRNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTST 373

Qy          85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144
               |||||||||||||||||||||||||||||| | |||| |||||||||||||:||||||
Db         374 VEACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAM 433

Qy         145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204
               |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db         434 NAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHA 493

Qy         205 FRIRAVTIDRMMSYLNSS 222
               |||||||:|||||||:|
Db         494 FRIRAVTINRMMSYLNAS 511


RESULT 14
US-09-917-265-39
; Sequence 39, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-39

  Query Match             82.4%;  Score 930;  DB 10;  Length 533;
  Best Local Similarity   91.9%;  Pred. No. 6.2e-83;
  Matches  182;  Conservative    8;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 84
               :|:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db         336 SRNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTST 395

Qy          85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144
               |||||||||||||||||||||||||||||| | |||| |||||||||||||:||||||
Db         396 VEACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAM 455

Qy         145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204
               |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db         456 NAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHA 515

Qy         205 FRIRAVTIDRMMSYLNSS 222
               |||||||:|||||||:|
Db         516 FRIRAVTINRMMSYLNAS 533


RESULT 15
US-09-917-265-36
; Sequence 36, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-36

  Query Match             82.4%;  Score 929;  DB 10;  Length 197;
  Best Local Similarity   92.4%;  Pred. No. 1.9e-83;
  Matches  182;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85
               |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db           1 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 60

Qy          86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145
               |||||||||||||||||||||||||||||| | |||| |||||||||||||:||||||
Db          61 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 120

Qy         146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205
               ||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Db         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 180

Qy         206 RIRAVTIDRMMSYLNSS 222
               |||||||:|||||||:|
Db         181 RIRAVTINRMMSYLNAS 197


Search completed: July 15, 2003, 11:11:42
Job time : 11.3649 secs
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 10:34:53 ; Search time 1015.52 Seconds
(without alignments)
9425.275 Million cell updates/sec

Title: US-09-917-265-49
Perfect score: 591
Sequence: 1 aggagcctccccacagcctc.....tgagttatctgaattcttcc 591

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
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8: em_htc:*
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10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	41	6.9	447	13	BI824638	BI824638 603033580
c	2	40	6.8	1099	13	BI523344	BI523344 603175938
	3	31	5.2	589	9	AI050362	AI050362 ub30a07.r
	4	30	5.1	373	12	BF552757	BF552757 UI-R-C0-i
	5	29	4.9	832	13	BI523569	BI523569 603175938
	6	26	4.4	342	13	BM257856	BM257856 521721 MA
	7	26	4.4	812	12	BG702253	BG702253 602683459
c	8	21	3.6	489	17	AQ393691	AQ393691 CITBI-E1-
	9	21	3.6	679	14	BU002107	BU002107 QGG30D21.
	10	21	3.6	726	17	BH728255	BH728255 BOMIG81TR
c	11	21	3.6	733	17	AQ631366	AQ631366 RPCI-11-4
	12	21	3.6	853	17	BH246749	BH246749 BOGAA09TR
c	13	20	3.4	241	17	AZ891891	AZ891891 RPCI-24-2
	14	20	3.4	340	17	AQ373901	AQ373901 RPCI11-14
c	15	20	3.4	385	12	BE703854	BE703854 MR2-NN111
	16	20	3.4	421	17	AQ673149	AQ673149 HS_5496_A
	17	20	3.4	511	9	AA135692	AA135692 zl11c04.r
c	18	20	3.4	516	17	AQ478437	AQ478437 RPCI-11-2
	19	20	3.4	581	14	BQ508151	BQ508151 EST615566
c	20	20	3.4	604	14	W63576	W63576 zc55h09.r1
	21	20	3.4	673	13	BM427122	BM427122 pgf2n.pk0
	22	20	3.4	711	14	BQ509384	BQ509384 EST616799
	23	20	3.4	742	13	BI175859	BI175859 EST516942
	24	20	3.4	757	13	BI177417	BI177417 EST518362
	25	20	3.4	859	12	BE737982	BE737982 601572557
c	26	19	3.2	247	10	BB425487	BB425487 BB425487
	27	19	3.2	259	10	BE604331	BE604331 WHE1405-1
	28	19	3.2	284	10	BB150477	BB150477 BB150477
	29	19	3.2	286	14	BQ392367	BQ392367 NISC_mq24
c	30	19	3.2	287	9	AL777805	AL777805 AL777805
	31	19	3.2	314	9	AL643008	AL643008 AL643008
	32	19	3.2	317	14	BQ392345	BQ392345 NISC_mq23
c	33	19	3.2	318	9	AL640225	AL640225 AL640225
	34	19	3.2	334	14	BQ392422	BQ392422 NISC_mq24
	35	19	3.2	383	13	BM073038	BM073038 MEST59-C0
c	36	19	3.2	402	17	AQ207082	AQ207082 HS_3235_A
	37	19	3.2	421	14	BQ394236	BQ394236 NISC_ng08
c	38	19	3.2	452	9	AU173260	AU173260 AU173260
	39	19	3.2	471	14	BQ523107	BQ523107 NISC_nl20
c	40	19	3.2	473	9	AL677765	AL677765 AL677765
	41	19	3.2	485	14	BQ395688	BQ395688 NISC_ng16
	42	19	3.2	491	14	BQ395792	BQ395792 NISC_ng17
c	43	19	3.2	492	9	AL783713	AL783713 AL783713
c	44	19	3.2	511	9	AL627756	AL627756 AL627756
	45	19	3.2	514	17	AQ141318	AQ141318 HS_3150_A

ALIGNMENTS

RESULT 1
BI824638
LOCUS BI824638 447 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5', mRNA sequence.
ACCESSION BI824638
VERSION BI824638.1 GI:15936188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11435 row: o column: 19
High quality sequence start: 3
High quality sequence stop: 445.
FEATURES Location/Qualifiers

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    source          1. .447
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5175018"
                    /clone_lib="NIH_MGC_115"
                    /lab_host="DH10B"
                    /note="Organ: pooled brain, lung, testis; Vector:
                    pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                    source anonymous pool of 6 male brains, age range 23-27; 1
                    male lung, age 27; and 1 male testis, age 69.  Library is
                    oligo-dT primed and directionally cloned (EcoRV site is
                    destroyed upon  cloning).  Average insert size 1.8 kb,
                    insert size range 1-3 kb. Library is normalized and
                    enriched for full-length clones and was  constructed by C.
                    Gruber (Invitrogen).  Research Genetics tracking  code
                    021. Note: this is a NIH_MGC Library."
BASE COUNT      149 a     63 c     87 g    148 t
ORIGIN

  Query Match             6.9%;  Score 41;  DB 13;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-12;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        508 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              |||||||||||||||||||||||||||||||||||||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 41


RESULT 2
BI523344/c
LOCUS       BI523344               1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES            Location/Qualifiers
     source         1. .1099
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5240216"
                    /clone_lib="NIH_MGC_121"
                    /lab_host="DH10B"
                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                    fetal brains, female age 20 weeks, female age 24 weeks,
                    and male age 26 weeks.  Library is oligo-dT primed and
                    directionally cloned (EcoRV site is destroyed  upon
                    cloning).  Average insert size 1.7 kb, insert size range
                    0.7-3.5 kb.  Library is normalized and enriched for
                    full-length clones and  was constructed by C. Gruber
                    (Invitrogen).  Research Genetics  tracking code 017. Note:
                    this is a NIH_MGC Library."
BASE COUNT      359 a     244 c     218 g     276 t      2 others
ORIGIN

  Query Match             6.8%;  Score 40;  DB 13;  Length 1099;
  Best Local Similarity   100.0%;  Pred. No. 4e-11;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        509 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              ||||||||||||||||||||||||||||||||||||||||
Db        524 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 485


RESULT 3
AI050362
LOCUS       AI050362               589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES            Location/Qualifiers
     source         1. .589
                    /organism="Mus musculus"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:1379220"
                    /clone_lib="Soares_thymus_2NbMT"
                    /sex="male"
                    /tissue_type="Thymus"
                    /dev_stage="4 weeks"
                    /lab_host="DH10B"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                    was primed with a Not I - oligo(dT) primer [5'
                    TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTT
                    3']; double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Not I and cloned into the Not I
                    and Eco RI sites of the modified pT7T3 vector. RNA
                    provided by Dr. Bertrand Jordan. Library went through two
                    rounds of normalization, and was constructed by Bento
                    Soares and M.Fatima Bonaldo."
BASE COUNT      162 a     159 c     142 g     126 t
ORIGIN

  Query Match             5.2%;  Score 31;  DB 9;  Length 589;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-06;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy        310 AGCATCTATGAGGACTTGAAGATGTACCAGA 340
              |||||||||||||||||||||||||||||||
Db        324 AGCATCTATGAGGACTTGAAGATGTACCAGA 354


RESULT 4
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /clone_lib="UI-R-C0"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0
                     library is a subtracted library derived from the UI-R-A1
                     and UI-R-E1 libraries. The UI-R-A1 library consisted of a
                     mixture of individually tagged normalized libraries
                     constructed from rat  placenta, adult lung, brain, liver,
                     kidney, heart, spleen, ovary,  and muscle. The UI-R-E1
                     library  consisted of a mixture of individually tagged
                     normalized libraries constructed from 8, 12 and 18-day
                     embryo. The tag is a string of 3-5 nucleotides present
                     between the Not I  site and the oligo-dT track which
                     allows identification of the library of origin of a clone
                     within the mixture. The subtracted library (UI-R-C0) was
                     constructed as follows: PCR amplified cDNA inserts from a
                     pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
                     been derived was used as a driver in a hybridization with
                     the pooled UI-R-A1 and UI-R-E1 library in the form of
                     single-stranded circles.  The remaining single-stranded
                     circles (subtracted library) was purified by
                     hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (Life Technologies) to generate the UI-R-C0
                     library. This procedure has been previously described
                     (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                     1996)"
BASE COUNT      106 a     93 c     89 g     85 t
ORIGIN
```

```
  Query Match             5.1%;  Score 30;  DB 12;  Length 373;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        310 AGCATCTATGAGGACTTGAAGATGTACCAG 339
              ||||||||||||||||||||||||||||||
Db         98 AGCATCTATGAGGACTTGAAGATGTACCAG 127


RESULT 5
BI523569
LOCUS       BI523569                832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: 1  column: 09
            High quality sequence start: 23
            High quality sequence stop: 821.
FEATURES             Location/Qualifiers
     source          1. .832
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      220 a    233 c    200 g    179 t
ORIGIN
```

```
  Query Match             4.9%;  Score 29;  DB 13;  Length 832;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-05;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GAAGAGATTGATCATGAAGATATCACAAA 161
              |||||||||||||||||||||||||||||
Db        520 GAAGAGATTGATCATGAAGATATCACAAA 548


RESULT 6
BM257856
LOCUS       BM257856                342 bp    mRNA    linear   EST 17-DEC-2001
DEFINITION  521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BM257856
VERSION     BM257856.1  GI:17893455
```

```
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 125  row: E  column: 18
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .342
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 3BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from marrow, alveolar
                     macrophage, ovary, fetal semitendonosus muscle, and fetal
                     longissimus muscle."
BASE COUNT       67 a    135 c     74 g     66 t
ORIGIN

  Query Match             4.4%;  Score 26;  DB 13;  Length 342;
  Best Local Similarity   100.0%;  Pred. No. 0.0027;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CAGAAGGCCAGACAAACTCTAGAATT 116
              ||||||||||||||||||||||||||
Db        294 CAGAAGGCCAGACAAACTCTAGAATT 319


RESULT 7
BG702253
LOCUS       BG702253                812 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
            mRNA sequence.
ACCESSION   BG702253
VERSION     BG702253.1  GI:13973409
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10714  row: e  column: 15
            High quality sequence stop: 804.
FEATURES             Location/Qualifiers
     source          1. .812
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4816118"
                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for  full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health).  Note: this is a NIH_MGC Library."
BASE COUNT      188 a    249 c    226 g    149 t
ORIGIN

  Query Match             4.4%;  Score 26;  DB 12;  Length 812;
  Best Local Similarity   100.0%;  Pred. No. 0.0037;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CAGAAGGCCAGACAAACTCTAGAATT 116
              ||||||||||||||||||||||||||
Db        573 CAGAAGGCCAGACAAACTCTAGAATT 598


RESULT 8
AQ393691/c
LOCUS       AQ393691                489 bp    DNA     linear   GSS 06-MAR-1999
DEFINITION  CITBI-E1-2544N3.TF CITBI-E1 Homo sapiens genomic clone 2544N3, DNA
            sequence.
ACCESSION   AQ393691
VERSION     AQ393691.1  GI:4364714
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2544N3.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .489
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2544N3"
```

```
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT      148 a     97 c    103 g    140 t      1 others
ORIGIN

  Query Match             3.6%;  Score 21;  DB 17;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        212 ATGAGAGTTGCCTGGCTTCCA 232
              |||||||||||||||||||||
Db        441 ATGAGAGTTGCCTGGCTTCCA 421


RESULT 9
BU002107
LOCUS       BU002107                679 bp    mRNA    linear   EST 22-AUG-2002
DEFINITION  QGG30D21.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGG30D21, mRNA sequence.
ACCESSION   BU002107
VERSION     BU002107.1  GI:22436502
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            singleton, see http://cgpdb.ucdavis.edu/ for details.
            Plate: QGG30  row: D  column: 21.
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Lactuca sativa"
                     /cultivar="L.serriola"
                     /db_xref="taxon:4236"
                     /clone="QGG30D21"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=flowers pre-fertilized
                     TAG_SEQ=GCTTGACGGG"
BASE COUNT      175 a    163 c    113 g    228 t
ORIGIN

  Query Match             3.6%;  Score 21;  DB 14;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        198 GGAATTAACCATGAATGAGAG 218
              |||||||||||||||||||||
Db          8 GGAATTAACCATGAATGAGAG 28


RESULT 10
BH728255
LOCUS       BH728255                726 bp    DNA     linear   GSS 20-FEB-2002
DEFINITION  BOMIG81TR BO_2_3_KB Brassica oleracea genomic clone BOMIG81, DNA
            sequence.
ACCESSION   BH728255
VERSION     BH728255.1  GI:18833650
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOMIG81TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .726
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOMIG81"
                     /clone_lib="BO_2_3_KB"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      171 a    194 c    172 g    189 t
ORIGIN

  Query Match             3.6%;  Score 21;  DB 17;  Length 726;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         45 CCTCAACCACTCCCAAAACCT 65
              |||||||||||||||||||||
Db        663 CCTCAACCACTCCCAAAACCT 683


RESULT 11
AQ631366/c
LOCUS       AQ631366                733 bp    DNA     linear   GSS 17-JUN-1999
DEFINITION  RPCI-11-482B16.TV RPCI-11 Homo sapiens genomic clone RPCI-11-482B16
            , DNA sequence.
ACCESSION   AQ631366
VERSION     AQ631366.1  GI:5094001
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 733)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
```

```
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .733
                      /organism="Homo sapiens"
                      /db_xref="GDB:7684743"
                      /db_xref="taxon:9606"
                      /clone="RPCI-11-482B16"
                      /clone_lib="RPCI-11"
                      /sex="Male"
                      /cell_type="Lymphocytes"
                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                      RPCI11 Human Male BAC Library"
BASE COUNT      223 a    127 c    133 g    250 t
ORIGIN

  Query Match             3.6%;  Score 21;  DB 17;  Length 733;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        494 ATTTTTATAAAACTAAAATCA 514
              |||||||||||||||||||||
Db        145 ATTTTTATAAAACTAAAATCA 125


RESULT 12
BH246749
LOCUS       BH246749                853 bp    DNA     linear   GSS 26-NOV-2001
DEFINITION  BOGAA09TR BOGA Brassica oleracea genomic clone BOGAA09, DNA
            sequence.
ACCESSION   BH246749
VERSION     BH246749.1  GI:17067298
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOGAA09TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES              Location/Qualifiers
     source           1. .853
                      /organism="Brassica oleracea"
                      /strain="TO1000DH3"
                      /db_xref="taxon:3712"
                      /clone="BOGAA09"
                      /clone_lib="BOGA"
                      /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                      genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      204 a    228 c    206 g    215 t
ORIGIN

  Query Match             3.6%;  Score 21;  DB 17;  Length 853;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         45 CCTCAACCACTCCCAAAACCT 65
              |||||||||||||||||||||
Db        690 CCTCAACCACTCCCAAAACCT 710


RESULT 13
AZ891891/c
LOCUS       AZ891891                241 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-24-201J11.TV RPCI-24 Mus musculus genomic clone RPCI-24-201J11
            , DNA sequence.
ACCESSION   AZ891891
VERSION     AZ891891.1  GI:13210836
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 241)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 201  row: J  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .241
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-24-201J11"
                      /clone_lib="RPCI-24"
                      /sex="Male"
                      /cell_type="Spleen/Brain"
                      /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                      RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                      library was  cloned in the pTARBAC1 cloning vector at the
                      BamH1 sites using MboI  partially digested male C57BL/6J
                      DNA."
BASE COUNT       57 a     39 c     35 g    110 t
ORIGIN

  Query Match             3.4%;  Score 20;  DB 17;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        494 ATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||
Db         20 ATTTTTATAAAACTAAAATC 1


RESULT 14
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```
AQ373901
LOCUS       AQ373901                340 bp    DNA     linear   GSS 20-MAY-1999
DEFINITION  RPCI11-145D9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-145D9,
            DNA sequence.
ACCESSION   AQ373901
VERSION     AQ373901.1  GI:4344924
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI11-145D9.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /db_xref="GDB:7555376"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-145D9"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT      122 a     61 c     41 g    116 t
ORIGIN

  Query Match             3.4%;  Score 20;  DB 17;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 AAGATATCACAAAGGATAAA 168
              ||||||||||||||||||||
Db         24 AAGATATCACAAAGGATAAA 43


RESULT 15
BE703854/c
LOCUS       BE703854                385 bp    mRNA    linear   EST 12-SEP-2000
DEFINITION  MR2-NN1112-090800-009-h11 NN1112 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE703854
VERSION     BE703854.1  GI:10091596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 385)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR2-NN1112-090
            800-009-h11&t3=2000-08-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 20
            High quality sequence stop: 358.
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NN1112"
                     /dev_stage="Adult"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       83 a    113 c    114 g     75 t
ORIGIN

  Query Match             3.4%;  Score 20;  DB 12;  Length 385;
  Best Local Similarity   100.0%;  Pred. No. 7.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 CTTCCAGAGAGATCTCTTTG 246
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Db         71 CTTCCAGAGAGATCTCTTTG 52


Search completed: July 16, 2003, 15:58:20
Job time : 1016.52 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:16:38 ; Search time 31.386 Seconds
(without alignments)
5774.736 Million cell updates/sec

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Perfect score: 591
Sequence: 1 aggagcctccccacagcctc.....tgagttatctgaattcttcc 591

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	488	82.6	669	4	US-09-079-984A-2	Sequence 2, Appli
3	59	10.0	660	1	US-08-186-529-3	Sequence 3, Appli
4	59	10.0	660	1	US-08-640-386A-3	Sequence 3, Appli
5	59	10.0	721	2	US-08-184-009-199	Sequence 199, App
6	59	10.0	721	2	US-08-458-356-199	Sequence 199, App
7	59	10.0	721	4	US-08-460-736-199	Sequence 199, App
8	59	10.0	752	4	US-08-848-760B-21	Sequence 21, Appl
9	59	10.0	1026	2	US-08-751-767A-1	Sequence 1, Appli
10	59	10.0	1316	2	US-08-684-687-3	Sequence 3, Appli
11	59	10.0	1316	4	US-09-851-520-3	Sequence 3, Appli
12	59	10.0	1364	1	US-08-265-087-3	Sequence 3, Appli
13	59	10.0	1364	1	US-08-621-493-3	Sequence 3, Appli
14	59	10.0	1364	2	US-08-965-688-3	Sequence 3, Appli
15	59	10.0	1364	4	US-09-260-173-3	Sequence 3, Appli
16	59	10.0	1560	2	US-08-751-767A-11	Sequence 11, Appl
17	59	10.0	1623	2	US-08-751-767A-9	Sequence 9, Appli
18	59	10.0	1645	4	US-09-310-842-2	Sequence 2, Appli
19	59	10.0	6139	2	US-08-751-767A-7	Sequence 7, Appli
20	31	5.2	713	2	US-08-385-335A-10	Sequence 10, Appl
21	31	5.2	6295	2	US-08-659-206A-4	Sequence 4, Appli
22	31	5.2	7287	2	US-08-659-206A-1	Sequence 1, Appli
c 23	27	4.6	39	4	US-09-079-984A-16	Sequence 16, Appl
c 24	20	3.4	20	3	US-08-621-841-52	Sequence 52, Appl
c 25	20	3.4	20	4	US-09-851-520-28	Sequence 28, Appl
c 26	20	3.4	20	4	US-09-851-520-31	Sequence 31, Appl
c 27	20	3.4	20	4	US-09-851-520-58	Sequence 58, Appl
c 28	19	3.2	20	4	US-09-851-520-59	Sequence 59, Appl
c 29	18	3.0	20	4	US-09-851-520-57	Sequence 57, Appl
c 30	18	3.0	409	4	US-09-189-060B-13	Sequence 13, Appl
31	18	3.0	415	4	US-09-189-060B-15	Sequence 15, Appl
32	18	3.0	4456	4	US-09-095-443-1	Sequence 1, Appli
33	17	2.9	20	1	US-08-012-543-13	Sequence 13, Appl
c 34	17	2.9	20	4	US-09-851-520-32	Sequence 32, Appl
c 35	17	2.9	20	4	US-09-851-520-39	Sequence 39, Appl
c 36	17	2.9	20	4	US-09-851-520-50	Sequence 50, Appl
c 37	17	2.9	20	4	US-09-851-520-56	Sequence 56, Appl
38	17	2.9	21	1	US-08-012-543-20	Sequence 20, Appl
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c 40	17	2.9	826	1	US-08-631-200-10	Sequence 10, Appl
c 41	17	2.9	826	1	US-08-829-553-10	Sequence 10, Appl
c 42	17	2.9	826	2	US-08-922-267A-10	Sequence 10, Appl
c 43	17	2.9	826	2	US-08-936-707A-10	Sequence 10, Appl
c 44	17	2.9	826	2	US-08-936-706A-10	Sequence 10, Appl
c 45	17	2.9	826	3	US-09-248-203-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,984A
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: Canine IL12
; LOCATION: 1 to 666
; IDENTIFICATION METHOD: Similarity
US-09-079-984A-12

Query Match 95.9%; Score 567; DB 4; Length 669;

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Qy         445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
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Db         520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

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Db         640 AGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 2
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; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

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Qy         325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
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Db         400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy         385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
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Qy         445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
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Db         520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy         505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 563
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RESULT 3
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
```

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;       STREET:  87 CambridgePark Drive
;       CITY:  Cambridge
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02140
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/186,529
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McDaniels, Patricia A.
;       REGISTRATION NUMBER:  33,194
;       REFERENCE/DOCKET NUMBER:  GI 5225
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-498-8401
;       TELEFAX:  617-876-5851
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  660 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       CELL TYPE:  Lymphoblast
;       CELL LINE:  RPMI 8866
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..660
US-08-186-529-3

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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 4
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

  Query Match             10.0%;  Score 59;  DB 1;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 5
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-199
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  Query Match             10.0%;  Score 59;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        617 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 675


RESULT 6
US-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-199

  Query Match             10.0%;  Score 59;  DB 2;  Length 721;
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Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        617 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 675


RESULT 7
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        617 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 675


RESULT 8
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
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;             FILING DATE: 09-APR-1997
;          ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;    INFORMATION FOR SEQ ID NO: 21:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;          MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;          SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-848-760B-21

  Query Match             10.0%;  Score 59;  DB 4;  Length 762;
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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        658 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 716


RESULT 9
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  170..826
US-08-751-767A-1

  Query Match             10.0%;  Score 59;  DB 2;  Length 1026;
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Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        725 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 783


RESULT 10
US-08-684-687-3
; Sequence 3, Application US/08684687
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  102..863
US-08-684-687-3

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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        759 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 817


RESULT 11
US-09-851-520-3
; Sequence 3, Application US/09851520
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; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

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Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        759 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 817


RESULT 12
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-265-087-3

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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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RESULT 13
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

  Query Match            10.0%;  Score 59;  DB 1;  Length 1364;
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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        758 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 816


RESULT 14
US-08-965-688-3
; Sequence 3, Application US/08965688
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; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3

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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        758 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 816


RESULT 15
US-09-260-173-3
; Sequence 3, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
;             STREET: Spring House Corporate Center, PO Box 457
;             CITY: Spring House
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/260,173
;             FILING DATE: 01-Mar-1999
;             CLASSIFICATION: <Unknown>
;                             17-JUN-1994
;                             18-APR-1994
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/965,688
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/265,087
;             FILING DATE: 17-JUN-1994
;             APPLICATION NUMBER: US 08/229,282
;             FILING DATE: 18-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: WST51AUSA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-540-9206
;             TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1364 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  101..859
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

  Query Match             10.0%;  Score 59;  DB 4;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 816


Search completed: July 16, 2003, 19:43:41
Job time : 32.386 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:21:13 ; Search time 111.898 Seconds
(without alignments)
8432.179 Million cell updates/sec

Title: US-09-917-265-49
Perfect score: 591
Sequence: 1 aggagcctccccacagcctc.....tgagttatctgaattcttcc 591

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1114047 seqs, 798260406 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		591	100.0	591	10	US-09-917-265-49	Sequence 49, Appl
2	c	591	100.0	591	10	US-09-917-265-51	Sequence 51, Appl
3		591	100.0	666	10	US-09-917-265-46	Sequence 46, Appl
4	c	591	100.0	666	10	US-09-917-265-48	Sequence 48, Appl
5		591	100.0	1455	10	US-09-917-265-104	Sequence 104, App
6	c	591	100.0	1455	10	US-09-917-265-106	Sequence 106, App
7		494	83.6	1533	10	US-09-917-265-66	Sequence 66, Appl
8	c	494	83.6	1533	10	US-09-917-265-68	Sequence 68, Appl
9		494	83.6	1599	10	US-09-917-265-61	Sequence 61, Appl
10	c	494	83.6	1599	10	US-09-917-265-63	Sequence 63, Appl
11		81	13.7	561	10	US-09-917-265-101	Sequence 101, App
12	c	81	13.7	561	10	US-09-917-265-103	Sequence 103, App
13		81	13.7	591	10	US-09-917-265-35	Sequence 35, Appl
14	c	81	13.7	591	10	US-09-917-265-37	Sequence 37, Appl
15		81	13.7	591	12	US-10-079-616-9	Sequence 9, Appli
16		81	13.7	666	10	US-09-917-265-32	Sequence 32, Appl
17	c	81	13.7	666	10	US-09-917-265-34	Sequence 34, Appl
18		81	13.7	1441	12	US-10-079-616-8	Sequence 8, Appli
19		81	13.7	1533	10	US-09-917-265-43	Sequence 43, Appl
20	c	81	13.7	1533	10	US-09-917-265-45	Sequence 45, Appl
21		81	13.7	1599	10	US-09-917-265-38	Sequence 38, Appl
22	c	81	13.7	1599	10	US-09-917-265-40	Sequence 40, Appl
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24		59	10.0	660	10	US-09-836-866-4	Sequence 4, Appli
25		59	10.0	689	12	US-10-079-616-26	Sequence 26, Appl
26		59	10.0	762	9	US-09-826-025-21	Sequence 21, Appl
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36		59	10.0	8644	10	US-09-828-825-13	Sequence 13, Appl
37		59	10.0	8659	10	US-09-828-825-11	Sequence 11, Appl
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40		24	4.1	39	10	US-09-917-265-91	Sequence 91, Appl
41	c	22	3.7	22	10	US-09-917-265-94	Sequence 94, Appl
42	c	20	3.4	558	9	US-10-198-846-12574	Sequence 12574, A
43	c	20	3.4	828	9	US-10-198-846-5002	Sequence 5002, Ap
44		20	3.4	63720	9	US-10-105-637-4	Sequence 4, Appli
45		19	3.2	6160	9	US-09-902-432-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION:
US-09-917-265-49

Query Match 100.0%; Score 591; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.3e-311;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

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Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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RESULT 2
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

  Query Match             100.0%;  Score 591;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-311;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        591 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 532

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Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 292

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Db         51 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 1


RESULT 3
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

  Query Match             100.0%;  Score 591;  DB 10;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-311;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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RESULT 4
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-48

Query Match 100.0%; Score 591; DB 10; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.3e-311;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        591 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Db        531 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 292

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        291 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 232

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 112

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db         51 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 1
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RESULT 5
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(897)
; OTHER INFORMATION:
US-09-917-265-104

Query Match 100.0%; Score 591; DB 10; Length 1455;
Best Local Similarity 100.0%; Pred. No. 1.3e-311;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db        367 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 426

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db        487 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 546

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 606

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 666

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 726

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 786

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 846

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 897


RESULT 6
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-106

  Query Match             100.0%;  Score 591;  DB 10;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-311;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 1090

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 1030

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 970

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 910

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 850

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 790

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 730

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 670

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 610

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 559


RESULT 7
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             83.6%;  Score 494;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-259;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 1069

Qy        128 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 1129

Qy        188 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 1189

Qy        248 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 1249

Qy        308 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 1309

Qy        368 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1310 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 1369

Qy        428 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1370 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 1429

Qy        488 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1430 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 1489

Qy        548 GTGCGGTGACCATC 561
              ||||||||||||||
Db       1490 GTGCGGTGACCATC 1503


RESULT 8
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
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;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             83.6%;  Score 494;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-259;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 465

Qy        128 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 405

Qy        188 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 345

Qy        248 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 285

Qy        308 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 225

Qy        368 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 165

Qy        428 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 105

Qy        488 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 45

Qy        548 GTGCGGTGACCATC 561
              ||||||||||||||
Db         44 GTGCGGTGACCATC 31


RESULT 9
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             83.6%;  Score 494;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-259;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 1135

Qy        128 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 1195

Qy        188 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 1255

Qy        248 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 1315

Qy        308 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 1375

Qy        368 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 1435

Qy        428 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 1495

Qy        488 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 1555

Qy        548 GTGCGGTGACCATC 561
              ||||||||||||||
Db       1556 GTGCGGTGACCATC 1569


RESULT 10
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             83.6%;  Score 494;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-259;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          68 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 127
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         524 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 465

Qy         128 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 187
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         464 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 405

Qy         188 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 247
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         404 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 345

Qy         248 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 307
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         344 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 285

Qy         308 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 367
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         284 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 225

Qy         368 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 427
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         224 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 165

Qy         428 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 487
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         164 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 105

Qy         488 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 547
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         104 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 45

Qy         548 GTGCGGTGACCATC 561
               ||||||||||||||
Db          44 GTGCGGTGACCATC 31
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RESULT 11
US-09-917-265-101
; Sequence 101, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
;   OTHER INFORMATION:
US-09-917-265-101

  Query Match            13.7%;  Score 81;  DB 10;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192

Qy         223 CTGGCTTCCAGAGAGATCTCT 243
               |||||||||||||||||||||
Db         193 CTGGCTTCCAGAGAGATCTCT 213
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RESULT 12
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-103

  Query Match            13.7%;  Score 81;  DB 10;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy         223 CTGGCTTCCAGAGAGATCTCT 243
               |||||||||||||||||||||
Db         369 CTGGCTTCCAGAGAGATCTCT 349
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RESULT 13
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-35

  Query Match            13.7%;  Score 81;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         223 CTGGCTTCCAGAGAGATCTCT 243
               |||||||||||||||||||||
Db         223 CTGGCTTCCAGAGAGATCTCT 243
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RESULT 14
US-09-917-265-37/c
; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-37

  Query Match             13.7%;  Score 81;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 15
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             13.7%;  Score 81;  DB 12;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
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Db        223 CTGGCTTCCAGAGAGATCTCT 243


Search completed: July 16, 2003, 19:58:54
Job time : 112.898 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:30:08 ; Search time 1071 Seconds
(without alignments)
8936.974 Million cell updates/sec

Title: US-09-917-265-49
Perfect score: 591
Sequence: 1 aggagcctccccacagcctc.....tgagttatctgaattcttcc 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	227.2	38.4	589	9	AI050362	AI050362 ub30a07.r
	2	222.2	37.6	812	12	BG702253	BG702253 602683459
c	3	210.2	35.6	1099	13	BI523344	BI523344 603175938
	4	188.8	31.9	373	12	BF552757	BF552757 UI-R-C0-i
	5	165.8	28.1	832	13	BI523569	BI523569 603175938
	6	94.2	15.9	342	13	BM257856	BM257856 521721 MA
	7	72.8	12.3	447	13	BI824638	BI824638 603033580
c	8	56.2	9.5	528	9	AI332701	AI332701 qq19a07.x
	9	39.2	6.6	912	12	BG770771	BG770771 602740813
	10	39	6.6	1042	17	CNS00BVZ	AL057907 Drosophil
	11	38.6	6.5	602	13	BM577222	BM577222 170006871
	12	38.2	6.5	579	9	AL783454	AL783454 AL783454
	13	38.2	6.5	906	10	BE537025	BE537025 601063459
	14	37.8	6.4	569	13	BI765729	BI765729 603046443
	15	37.8	6.4	599	12	BG714277	BG714277 602674965
	16	37.8	6.4	976	12	BE871124	BE871124 601447380
	17	37.2	6.3	407	14	T44964	T44964 8227 Lambda
	18	37.2	6.3	462	14	H76322	H76322 18027 Lambd
c	19	37	6.3	438	10	AW389687	AW389687 RC3-ST016
	20	36.8	6.2	726	17	CNS04HZF	AL291588 Tetraodon
	21	36.6	6.2	532	13	BI065861	BI065861 pgf1n.pk0
	22	36.6	6.2	583	13	BJ305783	BJ305783 BJ305783
	23	36.6	6.2	612	10	AV827486	AV827486 AV827486
c	24	36.6	6.2	617	13	BJ311377	BJ311377 BJ311377
	25	36.6	6.2	644	10	AV825194	AV825194 AV825194
	26	36.6	6.2	652	10	AV823245	AV823245 AV823245
	27	36.6	6.2	678	13	BJ317111	BJ317111 BJ317111
c	28	36.6	6.2	692	13	BJ322650	BJ322650 BJ322650
c	29	36.6	6.2	693	10	AV784178	AV784178 AV784178
	30	36.2	6.1	390	10	AW631037	AW631037 hh91b12.y
	31	36.2	6.1	484	14	T22900	T22900 4908 Lambda
	32	36.2	6.1	492	10	AW369275	AW369275 QV1-BN000
	33	36.2	6.1	628	13	BM011789	BM011789 603636162
	34	36.2	6.1	648	12	BG898673	BG898673 HOA3-1-H-
	35	36.2	6.1	707	13	BM046186	BM046186 603625949
	36	36.2	6.1	713	14	BM828150	BM828150 K-EST0100
	37	36.2	6.1	777	9	AU130730	AU130730 AU130730
	38	36.2	6.1	836	13	BI116347	BI116347 602869091
	39	36.2	6.1	1029	12	BE869200	BE869200 601445006
c	40	36	6.1	633	12	BE973158	BE973158 601652043
	41	35.8	6.1	181	9	AI938452	AI938452 sc45e07.y
	42	35.8	6.1	406	14	T22290	T22290 4298 Lambda
c	43	35.8	6.1	553	17	BH116430	BH116430 RPCI-24-3
	44	35.8	6.1	787	17	CNS010B7	AL098749 Drosophil
c	45	35.6	6.0	855	10	AW045087	AW045087 um17e11.y

ALIGNMENTS

RESULT 1
AI050362
LOCUS AI050362 589 bp mRNA linear EST 09-JUL-1998
DEFINITION ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35 subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION AI050362
VERSION AI050362.1 GI:3299479
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 589)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:901688
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 60.

FEATURES Location/Qualifiers
source 1. .589
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1379220"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 162 a 159 c 142 g 126 t
ORIGIN

Query Match 38.4%; Score 227.2; DB 9; Length 589;
Best Local Similarity 73.0%; Pred. No. 1.2e-57;
Matches 292; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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Qy         95 AGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATA 154
              |||||||| |||  ||  ||   |||||||||||| | ||||| || ||||||||||| |
Db        109 AGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGACA 168

Qy        155 TCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATG 214
              |||||  |||  |||||||||||| || || |||| |||||||||||| ||  || ||| |
Db        169 TCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAACG 228

Qy        215 AGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTG 274
              |||||||||||||| | |||||||  ||||  | ||| |  ||||| |||||| || |
Db        229 AGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCAC 288

Qy        275 GAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGT 334
                 ||| | ||||| |||| |  |||||||||| | ||||||||||||||||||||||||
Db        289 AGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGT 348

Qy        335 ACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCT 394
              ||||||  || ||| ||||||| ||||||   |||   |   |   | |   |||||||
Db        349 ACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATCA 408

Qy        395 TTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACA 454
              ||||  ||   |   |||||||    |  |||||||||||| | ||| | ||||||   ||
Db        409 TTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTGATGCAGTCTCTGAATCATAATG 468

Qy        455 GTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGA 494
              | | |||| |||  |||||| |  ||  ||  |||  | |
Db        469 GCGAGACTCTGCGCCAGAAACCTCCCTGTGGGGAGAAGCA 508
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RESULT 2
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.

FEATURES Location/Qualifiers
source 1. .812
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4816118"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 188 a 249 c 226 g 149 t
ORIGIN

Query Match 37.6%; Score 222.2; DB 12; Length 812;
Best Local Similarity 83.2%; Pred. No. 4.5e-56;
Matches 277; Conservative 0; Mismatches 53; Indels 3; Gaps 2;

```
Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||  |||||||||| ||||  |||||  ||||||||||
Db        483 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 542

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||  |||||||||||||  ||| ||||||||||||||||||||||||| ||
Db        543 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 602

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               | ||||||||  ||||||||  |||||||||||||||||||  ||||||||||||||||||
Db        603 CCTTGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 662

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||      |||||||||| |
Db        663 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGC--TAAATCCAGAGAGACC 720

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| ||||||||||||  |||  ||||| ||||||||||| |  ||||
Db        721 TCTTTCATAACTAATGGGAGTTGCCTGG-CTCCAGAAAGACCTCTTTTATGATGTGCCTG 779

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATG 333
              |||||||| || ||      ||   |  ||||||
Db        780 TGCCTTAGTAGTATTATGAAGACTTGAAAGATG 812
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RESULT 3
BI523344/c
LOCUS BI523344 1099 bp mRNA linear EST 29-AUG-2001
DEFINITION 603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3', mRNA sequence.
ACCESSION BI523344
VERSION BI523344.1 GI:15348136

```
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: 1  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      359 a    244 c    218 g    276 t      2 others
ORIGIN

  Query Match             35.6%;  Score 210.2;  DB 13;  Length 1099;
  Best Local Similarity   87.7%;  Pred. No. 2.2e-52;
  Matches  264;  Conservative    0;  Mismatches   33;  Indels    4;  Gaps    3;

Qy        294 GGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGC 353
              || ||||||| |||| || || ||||| ||| |||||||||||||| |||| |||||| |
Db        741 GGCCCTGTGCTTTAGTAGTATTTATGAAGAC-TGAAGATGTACCAGGTGGAGTTCAAGAC 683

Qy        354 CATGAACGCAAAGCTT-TTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGC 412
              |||||| ||||||||| | |||||||| ||||||||||||||||| ||||||||||||
Db        682 CATGAATGCAAAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGC 623

Qy        413 TGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGA 472
              || ||| ||| ||||||||| | |||||||||||||||||||||| |||||||||||| |
Db        622 TGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAA 563

Qy        473 AATCCTCCCTTGAAGAGCCGGAT--TTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 530
              ||||||||||||||| |||||| ||| |||||| |||||||||||||||||||||||||
Db        562 AATCCTCCCTTGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCT 503

Qy        531 TCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTC 590
              |||||||||||||||| || ||||| || |||||| ||||||| |||||||| ||||
Db        502 TCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTC 443

Qy        591 C 591
              |
Db        442 C 442


RESULT 4
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /clone_lib="UI-R-C0"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0
                     library is a subtracted library derived from the UI-R-A1
                     and UI-R-E1 libraries. The UI-R-A1 library consisted of a
                     mixture of individually tagged normalized libraries
                     constructed from rat  placenta, adult lung, brain, liver,
                     kidney, heart, spleen, ovary,  and muscle. The UI-R-E1
                     library  consisted of a mixture of individually tagged
                     normalized libraries constructed from 8, 12 and 18-day
                     embryo. The tag is a string of 3-5 nucleotides present
                     between the Not I  site and the oligo-dT track which
                     allows identification of the library of origin of a clone
                     within the mixture. The subtracted library (UI-R-C0) was
                     constructed as follows: PCR amplified cDNA inserts from a
                     pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
                     been derived was used as a driver in a hybridization with
                     the pooled UI-R-A1 and UI-R-E1 library in the form of
                     single-stranded circles.  The remaining single-stranded
                     circles (subtracted library) was purified by
                     hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (Life Technologies) to generate the UI-R-C0
                     library. This procedure has been previously described
                     (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                     1996)"
BASE COUNT      106 a     93 c     89 g     85 t
ORIGIN

  Query Match             31.9%;  Score 188.8;  DB 12;  Length 373;
  Best Local Similarity   69.6%;  Pred. No. 4.2e-46;
  Matches  256;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy        216 GAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGG 275
              ||| ||||||||| | | |||||  ||||  ||||  |  ||||| |||||| |  |
Db          4 GAGGTGCCTGGCTACTAAAGAGACTTCTTCCATAATAAGAGGGAGCTGCCTGCCTCCACA 63
```

```
Qy        276 AAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTA 335
              |||| | ||||| |||| |  ||||||||||| | ||||||||||||||||||||||||
Db         64 AAAGACTTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGTA 123

Qy        336 CCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTT 395
              ||||   || ||| |||||||| || |||   |||   |   |     |   |||||||
Db        124 CCAGTCAGAGTTCCAGGCCATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCAC 183

Qy        396 TCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAG 455
              ||||||   ||||||||||  ||||| ||||||||  | | | | ||||||  || | |
Db        184 TCTGGACAGAAACATGCTGATGGCTATTGATGAGCTAATGCGGTCTCTGAATCACAGCGG 243

Qy        456 TGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAA 515
              | || | |||  |||||| |  || | | |||  | |||  ||| | |   || || ||
Db        244 CGAGATTCTGCACCAGAAAGCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAA 303

Qy        516 GCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAG 575
              |||||| || || || ||||| ||||| |  || |   |||| ||| | ||  ||||||
Db        304 GCTCTGTATCCTGCTCCATGCCTTCAGCACACGCGTCATGACTATCAACAGGGTGATGAA 363

Qy        576 TTATCTGA 583
              ||||||||
Db        364 CTATCTGA 371
```

RESULT 5
BI523569
LOCUS BI523569 832 bp mRNA linear EST 29-AUG-2001
DEFINITION 603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5', mRNA sequence.
ACCESSION BI523569
VERSION BI523569.1 GI:15348361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 832)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11605 row: l column: 09
High quality sequence start: 23
High quality sequence stop: 821.
FEATURES Location/Qualifiers
source 1. .832
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5240216"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
BASE COUNT 220 a 233 c 200 g 179 t
ORIGIN

Query Match 28.1%; Score 165.8; DB 13; Length 832;
Best Local Similarity 87.1%; Pred. No. 5.4e-39;
Matches 182; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
Qy          2 GGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAA 61
              | | |||||||   ||| | ||   |||||||| ||||  |||||  ||||||||||||
Db        389 GAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAAA 448

Qy         62 ACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATT 121
              |||||||||| |||||||||||| ||| ||||||||||||||||||||||||||| ||
Db        449 ACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTACC 508

Qy        122 CCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGG 181
              | |||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        509 CTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGG 568

Qy        182 AGGCCTGCTTACCACTGGAATTAACCATG 210
              ||||||| |||||| |||||||||||| |
Db        569 AGGCCTGTTTACCATTGGAATTAACCAAG 597
```

RESULT 6
BM257856
LOCUS BM257856 342 bp mRNA linear EST 17-DEC-2001
DEFINITION 521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM257856
VERSION BM257856.1 GI:17893455
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 342)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 125 row: E column: 18
Seq primer: ATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .342
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
BASE COUNT 67 a 135 c 74 g 66 t
ORIGIN

Query Match 15.9%; Score 94.2; DB 13; Length 342;
Best Local Similarity 84.9%; Pred. No. 1.7e-17;

```
  Matches  118;  Conservative    0;  Mismatches   18;  Indels    3;  Gaps    1;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||  || || | ||||||||||    |   |||||| || |||||||
Db        207 AGGAGCCTCCCCACCACCACAGCAAGCCCAGGAAGGAGC---TGCCTCGACTACTCCCAA 263

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||  || |||||||||||||| |||||||||||||||||||||||||||  ||
Db        264 AACCTGCTGAGGGCTGTCAGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTAC 323

Qy        121 TCCTGCACTTCCGAAGAGA 139
              |||||||||||  || ||||
Db        324 TCCTGCACTTCTGAGGAGA 342


RESULT 7
BI824638
LOCUS       BI824638               447 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
            mRNA sequence.
ACCESSION   BI824638
VERSION     BI824638.1  GI:15936188
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11435  row: o  column: 19
            High quality sequence start: 3
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     source          1. .447
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5175018"
                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
BASE COUNT      149 a     63 c     87 g    148 t
ORIGIN

  Query Match             12.3%;  Score 72.8;  DB 13;  Length 447;
  Best Local Similarity   91.7%;  Pred. No. 5.9e-11;
  Matches   77;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        508 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGA 567
              |||||||||||||||||||||||||||||||||||||||||||| || ||||| || ||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGA 60

Qy        568 ATGATGAGTTATCTGAATTCTTCC 591
              ||||||| ||||||||| |||||
Db         61 GTGATGAGCTATCTGAATGCTTCC 84


RESULT 8
AI332701/c
LOCUS       AI332701               528 bp    mRNA    linear   EST 13-FEB-1999
DEFINITION  qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948
            3' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN
            );, mRNA sequence.
ACCESSION   AI332701
VERSION     AI332701.1  GI:4069260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1469   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 451.
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1932948"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      189 a     93 c     63 g    183 t
ORIGIN

  Query Match             9.5%;  Score 56.2;  DB 9;  Length 528;
  Best Local Similarity   88.4%;  Pred. No. 6.7e-06;
  Matches   61;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        523 ATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTG 582
              |||||||| ||||||||||||||||| || ||||| || |||||| ||||||| ||||||
Db        528 ATACTTCTCCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTG 469

Qy        583 AATTCTTCC 591
              ||| |||||
Db        468 AATGCTTCC 460


RESULT 9
BG770771
LOCUS       BG770771               912 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602740813F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4870730 5',
            mRNA sequence.
ACCESSION   BG770771
VERSION     BG770771.1  GI:14081424
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1744  row: i  column: 03
            High quality sequence start: 66
            High quality sequence stop: 503.
FEATURES             Location/Qualifiers
     source          1. .912
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4870730"
                     /clone_lib="NIH_MGC_49"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library. |"
BASE COUNT      218 a    344 c    237 g    112 t      1 others
ORIGIN

  Query Match             6.6%;  Score 39.2;  DB 12;  Length 912;
  Best Local Similarity   48.2%;  Pred. No. 1.2;
  Matches  110;  Conservative    0;  Mismatches  118;  Indels    0;  Gaps    0;

Qy        293 CGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGG 352
              ||| | || |||| | || | |  | |||||  |||  | |||| ||   ||||   |||
Db        138 CGGCCGTGCGCCTCATCACCCTGGAGGAGGAGATGACCAAGTACAAGCCCGAATCGGAGG 197

Qy        353 CCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGC 412
                |||  ||| ||    | |  ||   |       |   || |   ||   ||| || ||
Db        198 AGCTGACGGCAGAGAGGATCACAGAGTTCTGCCACCGCTTCCTGGAGGGCAAAATCAAGC 257

Qy        413 TGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGA 472
                  ||     |||||    ||| |  | |     |   ||| |  ||||
Db        258 CCCACCTGATGAGCCAGCTGCCGGAGGACTGGGACAAGCAGCCTGTCAAGGTGCTTGTTG 317

Qy        473 AATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCT 520
                  | | |||||   || |||| |    || | ||  ||  |||
Db        318 GGAAGAACTTCGAAGACGTGGCTTTTGACTGCACGACAAAAAACGTCT 365


RESULT 10
CNS00BVZ
LOCUS       CNS00BVZ                1042 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR24D11 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL057907
VERSION     AL057907.1  GI:4938170
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1042)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1042
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="BACR24D11"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
BASE COUNT      296 a    126 c     92 g    220 t    308 others
ORIGIN

  Query Match             6.6%;  Score 39;  DB 17;  Length 1042;
  Best Local Similarity   27.7%;  Pred. No. 1.4;
  Matches   74;  Conservative   43;  Mismatches  150;  Indels    0;  Gaps    0;

Qy        285 TTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGA 344
              ||| ||:|       :   |    |         | :   | | :| :  ::  |
Db        452 TTTNATSANANNNAANSNNAATNNTNAAATAAANNAANSNTNTNASSAASNTSSNAAANNT 511

Qy        345 ATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCA 404
                ||   |::         | |      ||      :  ||     | |           |
Db        512 NTTTSNGSSNSNTNTNANATAAAAAATANANANNSNNAAANAAAAAAAANAANNNNNNNNA 571

Qy        405 AAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGT 464
              ||| |       |         | |   :|||:     :| |:|| : |:::||:: :||
Db        572 AAANAAAAANSAAAASTNANNTTANNARTTASTAATTSTTAWTTSBTASWKTGWKTSTGA 631

Qy        465 GCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCAT 524
              :  | ||| ||: |: : |:||    :  : ||  ||: || ||  || | ::::
Db        632 KAGAGAGATATSTTSTSATSAATSTTSATWSTTSSATVTAAATASTATTATSMWSAAATS 691

Qy        525 ACTTCTTCATGCTTTCAGAATTCGTGC 551
              |:||::|:||   :|:  | | :: ::
Db        692 ASTTSYTSATATSWTSTAATTSSSSSS 718


RESULT 11
BM577222
LOCUS       BM577222                602 bp    mRNA    linear   EST 22-FEB-2002
DEFINITION  17000687163491 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
            19600449712899 5', mRNA sequence.
ACCESSION   BM577222
VERSION     BM577222.1  GI:18865689
KEYWORDS    EST.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
            ,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
```

```
  TITLE     Celera Anopheles gambiae EST project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Holt R.A.
            Celera Genomics
            45 w. Gude Dr., Rockville, MD 20850, USA
            Tel: 2404533151
            Fax: 2404534580
            Email: HoltRA@celera.com
            Plate: NU01004AWU  row: B  column: 21
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Anopheles gambiae"
                     /strain="RSP-ST (Reduced susc. to Permethrin - std.
                     chromosome)"
                     /db_xref="taxon:7165"
                     /clone="19600449712899"
                     /clone_lib="A.Gam.ad.cDNA.blood1"
                     /dev_stage="Adult"
                     /lab_host="DH10b"
                     /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
                     adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
                     hours  after human blood feeding. cDNA inserts >500 bp
                     cloned directionally  into pSport 1. Not 1 site is 3'.
                     Clones available through the Malaria  Research and
                     Reference Reagent Resource Center (www.malaria.mr4.org)"
BASE COUNT      201 a    124 c    149 g    128 t
ORIGIN

  Query Match             6.5%;  Score 38.6;  DB 13;  Length 602;
  Best Local Similarity   52.9%;  Pred. No. 1.5;
  Matches   83;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        317 ATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGG 376
              | ||||| ||   ||||||| | | | |||| |||   || |||||| |  || |   |
Db        151 AGGAGGATTTACGGATGTACGAAACGCAATTGAAGCTAATCAACGCAGAAATTATGGAGT 210

Qy        377 ATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTAC 436
              ||    ||  | ||| | |  | |||  || | ||  |   | |      ||   |||
Db        211 ATGTGCAGTTGAAGAACATGATCGATACAATCTTGGGGCAGGATCGACGCGAAGAGTTCA 270

Qy        437 AGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAA 473
              || | | |     || | ||| ||   ||     |||
Db        271 AGACGCAGGTCAACATCGGTGGGAACATGTTCATGAA 307


RESULT 12
AL783454
LOCUS       AL783454                579 bp    mRNA    linear   EST 25-JUN-2002
DEFINITION  AL783454 XGC-neurula Silurana tropicalis cDNA clone TNeu065k21 5',
            mRNA sequence.
ACCESSION   AL783454
VERSION     AL783454.1  GI:21569158
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2002
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Taylor R
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu065k21.p1cSP6
            Sequencing primer: P1CSP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1. .579
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="TNeu065k21"
                     /clone_lib="XGC-neurula"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT      179 a    141 c    150 g    109 t
ORIGIN

  Query Match             6.5%;  Score 38.2;  DB 9;  Length 579;
  Best Local Similarity   58.3%;  Pred. No. 2;
  Matches   67;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy        362 CAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTA 421
              ||||||   |  | |  |   |    ||| | ||  |||    |||| ||||| ||||
Db        104 CAAAGCAACTTGTAGCCCAGTATGAACAGGCCCTTAAGGAAATCAACAGGCTGAAAGCTC 163

Qy        422 TCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATC 476
                  |||| || | |||| ||||||   | |   ||  || | ||| ||||||
Db        164 AGTGTGAGGTGCTGCAGGACCTGAAGGCCGAGCCTGGCACGGGGCCCCAGAAACC 218


RESULT 13
BE537025
LOCUS       BE537025                906 bp    mRNA    linear   EST 09-AUG-2000
DEFINITION  601063459F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449847 5',
            mRNA sequence.
ACCESSION   BE537025
VERSION     BE537025.1  GI:9765670
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8427  row: e  column: 16
            High quality sequence stop: 665.
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3449847"
                     /clone_lib="NIH_MGC_10"
                     /cell_line="MGC36"
                     /lab_host="DH10B"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5 kb. Library prepared by Life
                     Technologies."
BASE COUNT      249 a    233 c    264 g    157 t      3 others
ORIGIN

  Query Match             6.5%;  Score 38.2;  DB 10;  Length 906;
  Best Local Similarity   59.8%;  Pred. No. 2.4;
  Matches   64;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;
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Qy        273 TGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGAT 332
              ||   |||||| ||| |  | ||  | | || ||||   ||    | |||| ||   ||
Db        334 TGTGGAGGCCTGTTTGAATAAGGAGCCGAGCTTTAGACCCACTGCTAAGGAGTTATTGAA 393

Qy        333 GTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATC 379
              | || || | |||| | | || ||||| | |||  |  || | || |
Db        394 GCACAAGTTTGAATACTACGCAATGAAAGAAAACTTCCTACTTGACC 440


RESULT 14
BI765729
LOCUS       BI765729                569 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603046443F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186675 5',
            mRNA sequence.
ACCESSION   BI765729
VERSION     BI765729.1  GI:15757307
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11466  row: e  column: 12
            High quality sequence start: 35
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5186675"
                     /clone_lib="NIH_MGC_116"
                     /lab_host="DH10B"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
BASE COUNT      112 a    171 c    182 g    104 t
ORIGIN

  Query Match             6.4%;  Score 37.8;  DB 13;  Length 569;
  Best Local Similarity   57.0%;  Pred. No. 2.6;
  Matches   69;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || ||   |||| | ||| | ||  ||||||| ||  ||| |   ||  ||| |||||
Db        290 AGAAGTGGCCCCTCTGCCCCTCCAGGCCCAGGCATGGTCCTGCTGCTTCACCCCTCCCCT 349

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||| | | | |     | ||| |||   ||    ||| |    | | || | |  |
Db        350 AGCCTGCCGTGTGGCACTGCCCACAGGCTGGGGACAAGCAGCCCTTGTGTTGAGTCAGGT 409

Qy        121 T 121
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Db        410 T 410
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RESULT 15
BG714277
LOCUS       BG714277                599 bp    mRNA    linear   EST 08-MAY-2001
DEFINITION  602674965F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797232 5',
            mRNA sequence.
ACCESSION   BG714277
VERSION     BG714277.1  GI:13993208
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10683  row: b  column: 17
            High quality sequence stop: 586.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4797232"
                     /clone_lib="NIH_MGC_96"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length  clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      146 a    171 c    183 g     99 t
ORIGIN

  Query Match             6.4%;  Score 37.8;  DB 12;  Length 599;
  Best Local Similarity   57.0%;  Pred. No. 2.6;
  Matches   69;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || ||   |||| | ||| | ||  ||||||| ||  ||| |   ||  ||| |||||
Db        255 AGAAGTGGCCCCTCTGCCCCTCCAGGCCCAGGCATGGTCCTGCTGCTTCACCCCTCCCCT 314

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||| | | | |     | ||| |||   ||    ||| |    | | || | |  |
Db        315 AGCCTGCCGTGTGGCACTGCCCACAGGCTGGGGACAAGCAGCCCTTGTGTTGAGTCAGGT 374

Qy        121 T 121
              |
Db        375 T 375


Search completed: July 16, 2003, 13:00:34
Job time : 1071 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 06:24:59 ; Search time 32.5883 Seconds
(without alignments)
5561.687 Million cell updates/sec

Title: US-09-917-265-49
Perfect score: 591
Sequence: 1 aggagcctccccacagcctc.....tgagttatctgaattcttcc 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	589.4	99.7	669	4	US-09-079-984A-12	Sequence 12, Appl
	2	583	98.6	669	4	US-09-079-984A-2	Sequence 2, Appli
	3	487	82.4	660	1	US-08-186-529-3	Sequence 3, Appli
	4	487	82.4	660	1	US-08-640-386A-3	Sequence 3, Appli
	5	487	82.4	762	4	US-08-848-760B-21	Sequence 21, Appl
	6	487	82.4	1316	2	US-08-684-687-3	Sequence 3, Appli
	7	487	82.4	1316	4	US-09-851-520-3	Sequence 3, Appli
	8	487	82.4	1364	1	US-08-265-087-3	Sequence 3, Appli
	9	487	82.4	1364	1	US-08-621-493-3	Sequence 3, Appli
	10	487	82.4	1364	2	US-08-965-688-3	Sequence 3, Appli
	11	487	82.4	1364	4	US-09-260-173-3	Sequence 3, Appli
	12	485.4	82.1	1645	4	US-09-310-842-2	Sequence 2, Appli
	13	483.8	81.9	721	2	US-08-184-009-199	Sequence 199, App
	14	483.8	81.9	721	2	US-08-458-356-199	Sequence 199, App
	15	483.8	81.9	721	4	US-08-460-736-199	Sequence 199, App
	16	483.8	81.9	1026	2	US-08-751-767A-1	Sequence 1, Appli
	17	483.8	81.9	1560	2	US-08-751-767A-11	Sequence 11, Appl
	18	483.8	81.9	1623	2	US-08-751-767A-9	Sequence 9, Appli
	19	483.8	81.9	6139	2	US-08-751-767A-7	Sequence 7, Appli
	20	303.2	51.3	713	2	US-08-385-335A-10	Sequence 10, Appl
	21	220.2	37.3	6295	2	US-08-659-206A-4	Sequence 4, Appli
	22	220.2	37.3	7287	2	US-08-659-206A-1	Sequence 1, Appli
	23	33.6	5.7	1545	1	US-07-872-673B-2	Sequence 2, Appli
	24	33.6	5.7	1696	4	US-09-198-603C-3	Sequence 3, Appli
	25	33.6	5.7	2454	1	US-07-872-673B-1	Sequence 1, Appli
c	26	32	5.4	7425	4	US-09-453-702B-212	Sequence 212, App
c	27	31.2	5.3	39	4	US-09-079-984A-6	Sequence 6, Appli
	28	31.2	5.3	169998	4	US-09-676-610B-24	Sequence 24, Appl
c	29	31	5.2	12886	4	US-09-453-702B-14	Sequence 14, Appl
	30	30.2	5.1	3900	2	US-08-356-060A-42	Sequence 42, Appl
	31	30.2	5.1	3900	4	US-08-460-900C-42	Sequence 42, Appl
	32	30.2	5.1	3900	4	US-08-674-509B-42	Sequence 42, Appl
	33	30.2	5.1	3900	4	US-08-954-698-42	Sequence 42, Appl
	34	30.2	5.1	3900	4	US-08-957-874-42	Sequence 42, Appl
	35	30.2	5.1	4434	2	US-08-540-406-5	Sequence 5, Appli
	36	30.2	5.1	4434	3	US-08-656-055-5	Sequence 5, Appli
	37	30.2	5.1	4434	4	US-08-954-668-5	Sequence 5, Appli
	38	30.2	5.1	4434	4	US-08-918-658-5	Sequence 5, Appli
	39	30.2	5.1	4434	5	PCT-US95-13233-5	Sequence 5, Appli
	40	29.6	5.0	895	4	US-09-221-017B-759	Sequence 759, App
c	41	29.6	5.0	903	2	US-08-874-347-9	Sequence 9, Appli
c	42	29.6	5.0	903	3	US-09-093-522-9	Sequence 9, Appli
	43	29.6	5.0	1318	3	US-09-183-253-3	Sequence 3, Appli
	44	29.6	5.0	2887	3	US-09-183-253-1	Sequence 1, Appli
	45	29.4	5.0	1737	4	US-09-173-151A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,984A
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: Canine IL12
; LOCATION: 1 to 666
; IDENTIFICATION METHOD: Similarity
US-09-079-984A-12

Query Match 99.7%; Score 589.4; DB 4; Length 669;

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  Best Local Similarity   99.8%;  Pred. No. 1.8e-186;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 2
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

  Query Match             98.6%;  Score 583;  DB 4;  Length 669;
  Best Local Similarity   99.2%;  Pred. No. 2.5e-184;
  Matches  586;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||| |||||||||| ||||||| |||||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666


RESULT 3
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
```

```
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-186-529-3

  Query Match             82.4%;  Score 487;  DB 1;  Length 660;
  Best Local Similarity   89.0%;  Pred. No. 2.3e-152;
  Matches  526;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| ||||  |||||  ||||||||||
Db         67 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| ||| ||||||||||||||||||||||||| ||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               | |||||||| |||||||||||||||||||||||||| |||||||||||||||||
Db        187 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||| |||||| |||||||||||| ||||||||||||||    |||||||||| |
Db        247 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 306

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| ||||||||||||||||  ||||| |||||||||||| || ||||
Db        307 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 366

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||| |||| |||||| |||||||
Db        367 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||| |||||||||||||| ||| |
Db        427 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 486

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||| | |||||||||||||||||||| |||||||||| |||||||||
Db        487 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||| || |||||| ||||||| |||||||| |||||
Db        607 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 657


RESULT 4
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

  Query Match             82.4%;  Score 487;  DB 1;  Length 660;
  Best Local Similarity   89.0%;  Pred. No. 2.3e-152;
  Matches  526;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| ||||  |||||  ||||||||||
Db         67 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| ||| ||||||||||||||||||||||||| ||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 186
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              | ||||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        187 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| |||||||||||||||   ||||||||||| |
Db        247 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 306

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| ||||||||||||||||  ||||| |||||||||||| || ||||
Db        307 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 366

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||||| |||| |||||| |||||||
Db        367 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||||| |||||||||||| |||||||||
Db        427 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 486

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||| | |||||||||||||||||||||| |||||||||||| |||||||||
Db        487 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||| || |||||| ||||||| ||||||||| |||||
Db        607 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 657
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RESULT 5
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
; GENERAL INFORMATION:
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: United States of America
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,760B
; FILING DATE: 25-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,702
; FILING DATE: 09-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PACE, DORAN R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: CNG-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-848-760B-21

Query Match 82.4%; Score 487; DB 4; Length 762;
Best Local Similarity 89.0%; Pred. No. 2.5e-152;
Matches 526; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| |||| |||||  ||||||||||
Db        169 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 228

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| ||| ||||||||||||||||||||||||||| ||
Db        229 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 288

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              | |||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        289 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 348

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| |||||||||||||||   |||||||||| |
Db        349 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 408

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| ||||||||||||||||  ||||| |||||||||||| || ||||
Db        409 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 468

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||||| |||| |||||| |||||||
Db        469 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 528

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||||| |||||||||||||| ||| |
Db        529 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 588

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||| | |||||||||||||||||||||| |||||||||||| |||||||||
Db        589 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 648

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 708

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||| || |||||| ||||||| ||||||||| |||||
Db        709 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 759
```

RESULT 6
US-08-684-687-3
; Sequence 3, Application US/08684687
; Patent No. 5830451
; GENERAL INFORMATION:
; APPLICANT: KIEFF, ELLIOTT D.
; APPLICANT: DEVERGNE, ODILE
; TITLE OF INVENTION: A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  102..863
US-08-684-687-3

  Query Match             82.4%;  Score 487;  DB 2;  Length 1316;
  Best Local Similarity   89.0%;  Pred. No. 3.4e-152;
  Matches  526;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| |||| |||||  ||||||||||
Db        270 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 329

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||  |||||||||||||  ||| ||||||||||||||||||||||||||
Db        330 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 389

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               | ||||||||  ||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        390 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 449

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| ||||||||||| ||||||||||||||   |||||||||| |
Db        450 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 509

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              |||||  ||||||||  ||||||||||||||||||  |||||  |||||||||||  || ||||
Db        510 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 569

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||  ||  ||  |||||  ||||||||||||||||||  ||||  ||||||  |||||||
Db        570 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 629

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||||  | ||||||||  ||||||||||||||||||  ||||||||||||||  ||| |
Db        630 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 689

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||  ||||||||||  |  ||||||||||||||||||||||  ||||||||||||  |||||||||
Db        690 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 749

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 809

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||  ||  |||||  ||  ||||||  |||||||  |||||||||  |||||
Db        810 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 860
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RESULT 7
US-09-851-520-3
; Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

  Query Match             82.4%;  Score 487;  DB 4;  Length 1316;
  Best Local Similarity   89.0%;  Pred. No. 3.4e-152;
  Matches  526;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| |||| |||||  ||||||||||
Db        270 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 329

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||  |||||||||||||  ||| ||||||||||||||||||||||||||  ||
Db        330 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 389

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               | ||||||||  ||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        390 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 449

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| ||||||||||| ||||||||||||||   |||||||||| |
Db        450 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 509

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              |||||  ||||||||  ||||||||||||||||||  |||||  |||||||||||  || ||||
Db        510 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 569

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||  ||  ||  |||||  ||||||||||||||||||  ||||  ||||||  |||||||
Db        570 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 629

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||||  | ||||||||  ||||||||||||||||||  ||||||||||||||  ||| |
Db        630 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 689

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||  ||||||||||  |  ||||||||||||||||||||||  ||||||||||||  |||||||||
Db        690 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 749

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 809

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||  ||  |||||  ||  ||||||  |||||||  |||||||||  |||||
Db        810 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 860
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RESULT 8
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
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;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-265-087-3

  Query Match             82.4%;  Score 487;  DB 1;  Length 1364;
  Best Local Similarity   89.0%;  Pred. No. 3.5e-152;
  Matches  526;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| |||  |||||  ||||||||||
Db        269 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 328

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| ||| ||||||||||||||||||||||||| ||
Db        329 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 388

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               | |||||||| |||||||||||||||||||||||||| ||||||||||||||||||
Db        389 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 448

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||||    |||||||||| |
Db        449 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 508

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| |||||||||||||||  ||||| |||||||||||| || ||||
Db        509 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 568

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||||| |||| |||||| |||||||
Db        569 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 628

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||| |||||||||||||| ||| |

Db        629 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 688

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||| | |||||||||||||||||||| |||||||||||| |||||||||
Db        689 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 748

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 808

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||| || |||||| ||||||| ||||||||| |||||
Db        809 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 859


RESULT 9
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

  Query Match             82.4%;  Score 487;  DB 1;  Length 1364;
  Best Local Similarity   89.0%;  Pred. No. 3.5e-152;
  Matches  526;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| |||  |||||  ||||||||||
Db        269 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 328
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Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||| ||| ||||||||||||||||||||||| ||
Db        329 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 388

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              | |||||||| |||||||||||||||||||||||||| ||||||||||||||||||
Db        389 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 448

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||||   |||||||||| |
Db        449 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 508

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| ||||||||||||||||  ||||| |||||||||||| || ||||
Db        509 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 568

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||| |||| |||||| |||||||
Db        569 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 628

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||| |||||||||||||| ||| |
Db        629 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 688

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||| | |||||||||||||||||| |||||||||| |||||||||
Db        689 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 748

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 808

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||| || |||||| ||||||| |||||||| |||||
Db        809 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 859


RESULT 10
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3

  Query Match             82.4%;  Score 487;  DB 2;  Length 1364;
  Best Local Similarity   89.0%;  Pred. No. 3.5e-152;
  Matches  526;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| |||| |||||  ||||||||||
Db        269 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 328

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| ||| ||||||||||||||||||||||| ||
Db        329 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 388

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              | |||||||| |||||||||||||||||||||||||| ||||||||||||||||||
Db        389 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 448

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||||   |||||||||| |
Db        449 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 508

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| ||||||||||||||||  ||||| |||||||||||| || ||||
Db        509 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 568

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||| |||| |||||| |||||||
Db        569 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 628

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||| |||||||||||||| ||| |
Db        629 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 688

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||| | |||||||||||||||||| |||||||||| |||||||||
Db        689 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 748

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 808

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||| || |||||| ||||||| |||||||| |||||
Db        809 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 859


RESULT 11
US-09-260-173-3
; Sequence 3, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
```

```
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1364 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  101..859
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

  Query Match             82.4%;  Score 487;  DB 4;  Length 1364;
  Best Local Similarity   89.0%;  Pred. No. 3.5e-152;
  Matches  526;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| ||||  |||||  ||||||||||
Db        269 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 328

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| ||| ||||||||||||||||||||||||| ||
Db        329 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 388

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               | |||||||| ||||||||||||||||||||||||| |||||||||||||||||
Db        389 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 448

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||||   |||||||||| |
Db        449 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 508

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| |||||||||||||||||  ||||| |||||||||||| || ||||
Db        509 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 568

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||||| |||| |||||| |||||||
Db        569 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 628

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||| |||||||||||||| ||| |

Db        629 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 688

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || ||||||||| | |||||||||||||||||||| |||||||||| |||||||||
Db        689 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 748

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 808

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||| || |||||| ||||||| ||||||||| |||||
Db        809 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 859


RESULT 12
US-09-310-842-2
; Sequence 2, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Ge
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1645
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1645)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
;   OTHER INFORMATION: Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
;   OTHER INFORMATION: position 1 to 2  can be modified with amino or caroxy
;   OTHER INFORMATION: features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1644)..(1645)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 164
;   OTHER INFORMATION: to 1645  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nuclei
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-2

  Query Match             82.1%;  Score 485.4;  DB 4;  Length 1645;
  Best Local Similarity   88.8%;  Pred. No. 1.3e-151;
  Matches  525;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||| ||||  |||||  ||||||||||
Db        801 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 860

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| ||| ||||||||||||||||||||||||| ||
Db        861 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 920

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               | |||||||| |||||||||||||||||||||||||| ||||||||||||||||||
Db        921 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 980

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        981 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 1040

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Db       1041 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 1100

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Db       1101 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 1160

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Db       1161 GCAAAACTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 1220

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Db       1221 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 1280

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Db       1281 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1340

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591

Db       1341 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 1391


RESULT 13
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-199

  Query Match             81.9%;  Score 483.8;  DB 2;  Length 721;
  Best Local Similarity   88.7%;  Pred. No. 2.8e-151;
  Matches  524;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Db        128 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 187

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Db        188 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 247

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Db        248 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 307

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Db        308 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 367

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Db        368 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 427

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Db        428 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 487

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Db        488 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 547

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Db        548 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 607

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Db        608 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 667

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591

Db        668 AGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 718


RESULT 14
US-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-199

  Query Match             81.9%;  Score 483.8;  DB 2;  Length 721;
  Best Local Similarity   88.7%;  Pred. No. 2.8e-151;
  Matches  524;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   ||||||||| |||| |||||  ||||||||||
Db        128 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 187

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||| |||||||||||||| ||| ||||||||||||||||||||||||||| ||
Db        188 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 247

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              | |||||||| |||||||||||||||||||||||||||| ||||||||||||||||||
Db        248 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 307

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||||   ||||||||||| |
Db        308 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 367

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| |||||||||||||||||  ||||| |||||||||||| || ||||
Db        368 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 427

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||||| |||| |||||| |||||||
Db        428 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 487

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||||| ||||||||||||||| ||| |
Db        488 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 547

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || ||||||||| | |||||||||||||||||||| |||||||||| ||||||||| |
Db        548 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 607

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 667

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||| || || ||| ||| ||| ||||||||| |||||
Db        668 AGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 718


RESULT 15
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

  Query Match             81.9%;  Score 483.8;  DB 4;  Length 721;
  Best Local Similarity   88.7%;  Pred. No. 2.8e-151;
  Matches  524;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   ||||||||| |||| |||||  ||||||||||
Db        128 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 187

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||| |||||||||||||| ||| ||||||||||||||||||||||||||| ||
Db        188 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 247

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              | |||||||| |||||||||||||||||||||||||||| ||||||||||||||||||
Db        248 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 307

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||||   ||||||||||| |
Db        308 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 367

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| |||||||||||||||||  ||||| |||||||||||| || ||||
Db        368 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 427

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||| || || ||||| |||||||||||||||||| |||| |||||| |||||||
Db        428 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 487

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||| |||||||||||||||||| ||||||||||||||| ||| |
Db        488 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 547

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || ||||||||| | |||||||||||||||||||| |||||||||| ||||||||| |
Db        548 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 607

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 667
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Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||| || ||||| || || ||| ||| ||| |||||||||| |||||
Db        668 AGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 718
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:38:23 ; Search time 115.652 Seconds
(without alignments)
8158.492 Million cell updates/sec

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Perfect score: 591
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1114047 seqs, 798260406 residues

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	591	100.0	591	10	US-09-917-265-51	Sequence 51, Appl
3	591	100.0	666	10	US-09-917-265-46	Sequence 46, Appl
c 4	591	100.0	666	10	US-09-917-265-48	Sequence 48, Appl
5	591	100.0	1455	10	US-09-917-265-104	Sequence 104, App
c 6	591	100.0	1455	10	US-09-917-265-106	Sequence 106, App
7	543	91.9	1533	10	US-09-917-265-66	Sequence 66, Appl
c 8	543	91.9	1533	10	US-09-917-265-68	Sequence 68, Appl
9	543	91.9	1599	10	US-09-917-265-61	Sequence 61, Appl
c 10	543	91.9	1599	10	US-09-917-265-63	Sequence 63, Appl
11	536.6	90.8	666	10	US-09-917-265-32	Sequence 32, Appl
c 12	536.6	90.8	666	10	US-09-917-265-34	Sequence 34, Appl
13	535	90.5	591	10	US-09-917-265-35	Sequence 35, Appl
c 14	535	90.5	591	10	US-09-917-265-37	Sequence 37, Appl
15	535	90.5	591	12	US-10-079-616-9	Sequence 9, Appli
16	535	90.5	1441	12	US-10-079-616-8	Sequence 8, Appli
17	525.4	88.9	689	12	US-10-079-616-26	Sequence 26, Appl
18	517.4	87.5	1533	10	US-09-917-265-43	Sequence 43, Appl
c 19	517.4	87.5	1533	10	US-09-917-265-45	Sequence 45, Appl
20	517.4	87.5	1599	10	US-09-917-265-38	Sequence 38, Appl
c 21	517.4	87.5	1599	10	US-09-917-265-40	Sequence 40, Appl
22	511.4	86.5	561	10	US-09-917-265-101	Sequence 101, App
c 23	511.4	86.5	561	10	US-09-917-265-103	Sequence 103, App
24	487	82.4	762	9	US-09-826-025-21	Sequence 21, Appl
25	487	82.4	1395	10	US-09-924-703-5	Sequence 5, Appli
26	487	82.4	8578	10	US-09-828-825-1	Sequence 1, Appli
27	487	82.4	8578	10	US-09-828-825-3	Sequence 3, Appli
28	487	82.4	8608	10	US-09-828-825-7	Sequence 7, Appli
29	487	82.4	8623	10	US-09-828-825-5	Sequence 5, Appli
30	487	82.4	8629	10	US-09-828-825-15	Sequence 15, Appl
31	487	82.4	8638	10	US-09-828-825-9	Sequence 9, Appli
32	487	82.4	8644	10	US-09-828-825-13	Sequence 13, Appl
33	487	82.4	8659	10	US-09-828-825-11	Sequence 11, Appl
34	485.4	82.1	1645	9	US-10-228-811-2	Sequence 2, Appli
35	483.8	81.9	660	10	US-09-754-014-6	Sequence 6, Appli
36	483.8	81.9	660	10	US-09-836-866-4	Sequence 4, Appli
37	483.8	81.9	1026	9	US-10-172-399-5	Sequence 5, Appli
38	349.4	59.1	660	10	US-09-754-014-8	Sequence 8, Appli
39	345.2	58.4	660	10	US-09-754-014-7	Sequence 7, Appli
40	303.2	51.3	1265	9	US-10-172-399-1	Sequence 1, Appli
41	71	12.0	79	12	US-10-079-616-24	Sequence 24, Appl
42	37.8	6.4	1316	10	US-09-070-927A-191	Sequence 191, App
43	36.2	6.1	445	9	US-09-918-995-35388	Sequence 35388, A
44	36.2	6.1	6577	10	US-09-880-107-2187	Sequence 2187, Ap
45	34.2	5.8	1714	9	US-10-242-056-60	Sequence 60, Appl

ALIGNMENTS

```
RESULT 1
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-49

  Query Match             100.0%;  Score 591;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-184;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591


RESULT 2
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

  Query Match             100.0%;  Score 591;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-184;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 292

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 232

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 112

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 1


RESULT 3
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

  Query Match             100.0%;  Score 591;  DB 10;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2e-184;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435
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Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 4
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-48

  Query Match            100.0%;  Score 591;  DB 10;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2e-184;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 292

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 232

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 112

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 1


RESULT 5
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
;   OTHER INFORMATION:
US-09-917-265-104

  Query Match            100.0%;  Score 591;  DB 10;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-184;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 366

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 426

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 486

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 546

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 606

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 666

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 726

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 786

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 846

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 897


RESULT 6
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-106

  Query Match            100.0%;  Score 591;  DB 10;  Length 1455;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-184;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 1090

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 1030

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 970

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 910

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 850

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 790

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 730

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 670

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 610

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 559


RESULT 7
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match            91.9%;  Score 543;  DB 10;  Length 1533;
  Best Local Similarity  94.9%;  Pred. No. 2.3e-168;
  Matches  561;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
                || | | | || ||  |  | ||   ||| || || ||||| ||  | ||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAA 1002

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
                | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 1062

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 1122

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 1242

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 1302

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 1422

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
                |||||||||||||||||||| ||||||||||   ||  |||| ||||||
Db       1483 AGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 8
US-09-917-265-68/c
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; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             91.9%;  Score 543;  DB 10;  Length 1533;
  Best Local Similarity   94.9%;  Pred. No. 2.3e-168;
  Matches  561;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | | | || ||  |  | ||   ||| || || ||||| ||  | ||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAA 532

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 292

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 232

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 112

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||| ||||||||||   ||  |||| ||||||
Db         51 AGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 9
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             91.9%;  Score 543;  DB 10;  Length 1599;
  Best Local Similarity   94.9%;  Pred. No. 2.3e-168;
  Matches  561;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | | | || ||  |  | ||   ||| || || ||||| ||  | ||||||||||||
Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAA 1068

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 ACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 1128

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 1188

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 1308

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 1368

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 1488

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||| ||||||||||   ||  |||| ||||||
Db       1549 AGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 10
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
```

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;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match            91.9%;  Score 543;  DB 10;  Length 1599;
  Best Local Similarity  94.9%;  Pred. No. 2.3e-168;
  Matches  561;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | | | || ||  |  | ||   ||| || || ||||| ||  | ||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAA 532

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTTATGACGGTCCTG 292

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 232

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 112

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||| ||||||||||   ||  |||| ||||||
Db         51 AGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 11
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-32

  Query Match            90.8%;  Score 536.6;  DB 10;  Length 666;
  Best Local Similarity  94.2%;  Pred. No. 1.8e-166;
  Matches  557;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||| |||||||||| || |||| |||||||||| |||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| ||||||||||||||||||||||||||||||||||||||||| ||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| ||||||||||||||||  |||| ||||||||||||||  ||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||| |||||||||||||||||||||||||| |||| ||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||||| |||||||||||||||||||||||||| ||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||| |||||||| |||||||||||||| ||||||||| |||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 12
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

  Query Match            90.8%;  Score 536.6;  DB 10;  Length 666;
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  Best Local Similarity   94.2%;  Pred. No. 1.8e-166;
  Matches  557;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| |||||||||||||||||||||||||||||||||||||||| ||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| |||||||||||||||||  ||||| ||||||||||||||  ||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||| |||||||||||||||||||||||||| ||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||| ||||||||| |||||||||||| ||||||||| |||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 13
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-35

  Query Match            90.5%;  Score 535;  DB 10;  Length 591;
  Best Local Similarity   94.1%;  Pred. No. 5.5e-166;
  Matches  556;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||| |||||||||| || |||| |||||||||| |||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| |||||||||||||||||||||||||||||||||||||||| ||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| |||||||||||||||||  ||||| ||||||||||||||  ||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||| |||||||||||||||||||||||||| ||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||| ||||||||| |||||||||||| ||||||||| |||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 14
US-09-917-265-37/c
; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-37

  Query Match            90.5%;  Score 535;  DB 10;  Length 591;
  Best Local Similarity   94.1%;  Pred. No. 5.5e-166;
  Matches  556;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| |||||||||||||||||||||||||||||||||||||||| ||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
               | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 15
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;             TELECOMMUNICATION INFORMATION:
;                  TELEPHONE: 202-628-5197
;                  TELEFAX: 202-737-3528
;        INFORMATION FOR SEQ ID NO: 9:
;             SEQUENCE CHARACTERISTICS:
;                  LENGTH: 591 base pairs
;                  TYPE: nucleic acid
;                  STRANDEDNESS: single
;                  TOPOLOGY: linear
;             MOLECULE TYPE: cDNA
;             SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             90.5%;  Score 535;  DB 12;  Length 591;
  Best Local Similarity   94.1%;  Pred. No. 5.5e-166;
  Matches  556;  Conservative    0;  Mismatches   35;  Indels   0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              || ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


Search completed: July 16, 2003, 13:16:25
Job time : 115.652 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:54:38 ; Search time 19.8032 Seconds
(without alignments)
1325.559 Million cell updates/sec

Title: US-09-917-265-50
Perfect score: 994
Sequence: 1 RSLPTASPSPGIFQCLNHSQ.....HAFRIRAVTIDRMMSYLNSS 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	994	100.0	197	20	AAW74325	Canine mature CLAF
2	994	100.0	222	19	AAW41793	Canine IL-12 P35 s
3	994	100.0	222	20	AAY02343	Canine Interleukin
4	994	100.0	222	20	AAW74324	Canine full length
5	994	100.0	222	20	AAW84374	Canine interleukin
6	994	100.0	222	22	AAG66483	Canine protein #4.
7	989	99.5	222	19	AAW41792	Canine IL-12 P35 s
8	989	99.5	222	20	AAY02340	Canine Interleukin
9	989	99.5	222	20	AAW84372	Canine interleukin
10	989	99.5	222	22	AAG66481	Canine protein #2.
11	932	93.8	197	19	AAW76176	Feline FLAFp35 mat
12	932	93.8	222	19	AAW76175	Feline FLAFp35 pro
13	893	89.8	219	22	AAE08609	Modified human cyt
14	888	89.3	219	22	AAE08606	Modified human cyt
15	888	89.3	219	22	AAE08613	Modified human cyt
16	883	88.8	219	22	AAE08610	Modified human cyt
17	883	88.8	219	22	AAE08612	Modified human cyt
18	878	88.3	219	22	AAE08611	Modified human cyt
19	875	88.0	219	16	AAR79187	Human interleukin-
20	875	88.0	219	19	AAW51222	Human interleukin-
21	875	88.0	253	17	AAW07399	Human interleukin-
22	875	88.0	253	18	AAW09780	Interleukin-12 p35
23	875	88.0	253	19	AAW62993	Human interleukin-
24	875	88.0	253	19	AAW44325	Heterodimeric huma
25	875	88.0	253	21	AAY44182	Human interleukin-
26	875	88.0	253	22	AAB67263	IL-12 vaccine adju
27	875	88.0	503	23	AAU76523	Anti-Interleukin-1
28	875	88.0	527	23	AAE19817	Human IL-12.1 prot
29	875	88.0	537	23	AAE19820	Human IL-12.2 prot
30	875	88.0	542	23	AAE19819	Human IL-12.3 prot
31	875	88.0	547	23	AAE19821	Human IL-12.4 prot
32	871	87.6	219	22	AAE08608	Modified human cyt
33	871	87.6	526	23	AAE19818	Human IL-12.0 prot
34	870	87.5	253	13	AAR23729	Natural killer cel
35	869	87.4	219	18	AAW24236	35 kDa subunit of
36	869	87.4	219	18	AAW36940	35 kDa subunit of
37	869	87.4	219	18	AAW36942	35 kDa subunit of
38	869	87.4	219	19	AAW58726	Cytotoxic lymphocy
39	869	87.4	219	19	AAW51312	Human Interleukin-
40	869	87.4	219	19	AAW57483	Human interleukin-
41	869	87.4	219	20	AAY42488	Human interleukin
42	869	87.4	219	21	AAB23795	Human interleukin
43	869	87.4	219	21	AAY54918	Human p35 protein
44	869	87.4	219	22	AAE08614	Human cytokine p35
45	868	87.3	219	22	AAE08607	Modified human cyt

ALIGNMENTS

RESULT 1
AAW74325
ID AAW74325 standard; Protein; 197 AA.
XX
AC AAW74325;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine mature CLAF p35 subunit.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP02295.
XX
PR 03-JUN-1997; 97JP-0161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Eda Y, Imamura T, Maeda H, Tokiyoshi S;
XX
DR WPI; 1999-070260/06.
DR N-PSDB; AAX18179.
XX
PT Canine cytokine protein which activates canine cytotoxic T
PT lymphocytes - is useful for treatment of viral and autoimmune

```
PT   diseases in dogs
XX
PS   Claim 1; Page 28-29; 51pp; Japanese.
XX
CC   This sequence is the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence   197 AA;

  Query Match             100.0%;  Score 994;  DB 20;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-98;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        181 RIRAVTIDRMMSYLNSS 197


RESULT 2
AAW41793
ID   AAW41793 standard; peptide; 222 AA.
XX
AC   AAW41793;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant.
XX
OS   Canis sp.
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   N-PSDB; AAV13819.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 3; Pages 11-12; 12pp; Japanese.
XX
CC   The present sequence is a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence   222 AA;

  Query Match             100.0%;  Score 994;  DB 19;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-98;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 3
AAY02343
ID   AAY02343 standard; Protein; 222 AA.
XX
AC   AAY02343;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Canine Interleukin-12 (IL-12) protein sequence.
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease.
XX
OS   Canis sp.
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   N-PSDB; AAX35626.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence represents canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
```

```
SQ   Sequence   222 AA;

  Query Match            100.0%;  Score 994;  DB 20;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-98;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 4
AAW74324
ID   AAW74324 standard; Protein; 222 AA.
XX
AC   AAW74324;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   N-PSDB; AAX18178.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 1; Page 26-28; 51pp; Japanese.
XX
CC   This sequence is the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence   222 AA;

  Query Match            100.0%;  Score 994;  DB 20;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-98;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 5
AAW84374
ID   AAW84374 standard; Protein; 222 AA.
XX
AC   AAW84374;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03163.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
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CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   222 AA;

  Query Match           100.0%;  Score 994;  DB 20;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-98;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 6
AAG66483
ID   AAG66483 standard; Protein; 222 AA.
XX
AC   AAG66483;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..25
FT                   /label= Signal_peptide
FT   Protein         26..222
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64389.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Disclosure; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   222 AA;

  Query Match           100.0%;  Score 994;  DB 22;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-98;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 7
AAW41792
ID   AAW41792 standard; peptide; 222 AA.
XX
AC   AAW41792;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant.
XX
OS   Canis sp.
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   N-PSDB; AAV13818.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 3; Page 9; 12pp; Japanese.
XX
CC   The present sequence is a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence   222 AA;

  Query Match           99.5%;  Score 989;  DB 19;  Length 222;
  Best Local Similarity  99.5%;  Pred. No. 3e-97;
  Matches  196;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||:||
Db        206 RIRAVTIDRMMSYLSSS 222


RESULT 8
AAY02340
ID   AAY02340 standard; Protein; 222 AA.
XX
AC   AAY02340;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Canine Interleukin-12 (IL-12) protein sequence.
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease.
XX
OS   Canis sp.
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   N-PSDB; AAX35616.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence represents canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence   222 AA;

  Query Match             99.5%;  Score 989;  DB 20;  Length 222;
  Best Local Similarity   99.5%;  Pred. No. 3e-97;
  Matches  196;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||:||
Db        206 RIRAVTIDRMMSYLSSS 222


RESULT 9
AAW84372
ID   AAW84372 standard; Protein; 222 AA.
XX
AC   AAW84372;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03153.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   222 AA;

  Query Match             99.5%;  Score 989;  DB 20;  Length 222;
  Best Local Similarity   99.5%;  Pred. No. 3e-97;
  Matches  196;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy         181 RIRAVTIDRMMSYLNSS 197
                |||||||||||||:||
Db         206 RIRAVTIDRMMSYLSSS 222


RESULT 10
AAG66481
ID   AAG66481 standard; Protein; 222 AA.
XX
AC   AAG66481;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..25
FT                   /label= Signal_peptide
FT   Protein         26..222
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64379.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   222 AA;

  Query Match             99.5%;  Score 989;  DB 22;  Length 222;
  Best Local Similarity   99.5%;  Pred. No. 3e-97;
  Matches  196;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy          61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy         181 RIRAVTIDRMMSYLNSS 197
                |||||||||||||:||
Db         206 RIRAVTIDRMMSYLSSS 222


RESULT 11
AAW76176
ID   AAW76176 standard; Protein; 197 AA.
XX
AC   AAW76176;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 mature protein.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   N-PSDB; AAV56629.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 10; Page 51; 94pp; Japanese.
XX
CC   This sequence repesents a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus.
XX
SQ   Sequence   197 AA;

  Query Match             93.8%;  Score 932;  DB 19;  Length 197;
  Best Local Similarity   92.9%;  Pred. No. 3.1e-91;
  Matches  183;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy           1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
                |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db           1 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 60

Qy          61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
                |||||||||||||||||||||||||||| | |||| |||||||||||||:||||||
Db          61 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 120

Qy         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
                |||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||||
Db         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 180

Qy         181 RIRAVTIDRMMSYLNSS 197
                |||||||:|||||||||
Db         181 RIRAVTINRMMSYLNSS 197
```

```
RESULT 12
AAW76175
ID   AAW76175 standard; Protein; 222 AA.
XX
AC   AAW76175;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 protein.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..25
FT                   /label= signal
FT   Protein         26..222
FT                   /label= FLAFp35
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   N-PSDB; AAV56628.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 8; Page 49-51; 94pp; Japanese.
XX
CC   This sequence represents a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence   222 AA;

  Query Match             93.8%;  Score 932;  DB 19;  Length 222;
  Best Local Similarity   92.9%;  Pred. No. 3.7e-91;
  Matches  183;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db         26 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||||||||||||||||||||||| | |||| |||||||||||||:||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:||||||||
Db        206 RIRAVTINRMMSYLNSS 222
```

```
RESULT 13
AAE08609
ID   AAE08609 standard; Protein; 219 AA.
XX
AC   AAE08609;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 from clone R2-571.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Leader_peptide
FT   Protein         23..219
FT                   /note= "Mature modified p35"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   N-PSDB; AAD15216.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 124; Fig 11; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein.
XX
SQ   Sequence   219 AA;

  Query Match             89.8%;  Score 893;  DB 22;  Length 219;
  Best Local Similarity   89.3%;  Pred. No. 5.3e-87;
  Matches  176;  Conservative    7;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||| |||||||| ||||||||||||||||||||
Db         23 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||  |||||||| |||||||||||| | |||| ||| ||||||||||:||| ||
Db         83 EACLPLELATNESCLASRGISLITNGSCLASRKTSFMTTLCLGSIYEDLKMYQVEFKTMN 142

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||:|||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        143 AKLLMNPKRQIFLDQNMLTAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202
```

```
Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:|||||||||
Db        203 RIRAVTINRMMSYLNSS 219


RESULT 14
AAE08606
ID   AAE08606 standard; Protein; 219 AA.
XX
AC   AAE08606;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 from clone R2-796.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Leader_peptide
FT   Protein         23..219
FT                   /note= "Mature modified p35"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   N-PSDB; AAD15213.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 124; Fig 11; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein.
XX
SQ   Sequence   219 AA;

  Query Match            89.3%;  Score 888;  DB 22;  Length 219;
  Best Local Similarity   88.8%;  Pred. No. 1.8e-86;
  Matches  175;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:||||||||||| ||||||||| ||||||||||||||||||||||
Db         23 RNLPVATPGPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||| ||||| ||| | ||||||||| | |||| ||||||||||||||:||| ||
Db         83 EACLPLELIKNESCLNSRETSFITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKTMN 142

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||:|||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        143 AKLLMNPKRQIFLDQNMLTAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:|||||||||
Db        203 RIRAVTINRMMSYLNSS 219


RESULT 15
AAE08613
ID   AAE08613 standard; Protein; 219 AA.
XX
AC   AAE08613;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 from clone R1-4-87.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Leader_peptide
FT   Protein         23..219
FT                   /note= "Mature modified p35"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   N-PSDB; AAD15220.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 124; Fig 11; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein.
XX
SQ   Sequence   219 AA;

  Query Match            89.3%;  Score 888;  DB 22;  Length 219;
  Best Local Similarity   88.8%;  Pred. No. 1.8e-86;
  Matches  175;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:||||||||||| ||||||||| ||||||||||||||||||||||
```

```
Db         23 RNLPVATPGPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||  ||||| ||| | |||||||||  | |||| |||||||||||||||:||| ||
Db         83 EACLPLELIKNESCLNSRETSFITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKTMN 142

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||:|||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        143 AKLLMNPKRQIFLDQNMLTAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:||||||||
Db        203 RIRAVTINRMMSYLNSS 219


Search completed: July 15, 2003, 11:02:51
Job time : 19.8032 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:49 ; Search time 8.63459 Seconds
(without alignments)
2193.328 Million cell updates/sec

Title: US-09-917-265-50
Perfect score: 994
Sequence: 1 RSLPTASPSPGIFQCLNHSQ.....HAFRIRAVTIDRMMSYLNSS 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	875	88.0	253	2	B38957	interleukin 12A pr
2	553	55.6	215	2	I56135	interleukin 12 p35
3	97.5	9.8	816	2	D84601	hypothetical prote
4	93	9.4	1583	2	F97846	hypothetical prote
5	90	9.1	615	2	T20187	hypothetical prote
6	88.5	8.9	383	2	F71550	probable endonucle
7	86.5	8.7	1134	2	S53955	hypothetical prote
8	86	8.7	1286	2	T16507	hypothetical prote
9	85.5	8.6	1957	2	T38077	hypothetical coile
10	85	8.6	1476	2	A41185	alpha-2 macroglobu
11	84.5	8.5	310	2	T33611	hypothetical prote
12	84	8.5	849	2	C97303	hypothetical prote
13	83	8.4	1061	2	JC7116	Xsal-3 protein - A
14	82.5	8.3	271	2	AB1292	amino acid ABC tra
15	82.5	8.3	523	2	D86492	hypothetical prote
16	82.5	8.3	523	2	D72130	hypothetical prote
17	82.5	8.3	607	2	D64603	hypothetical prote
18	82.5	8.3	640	2	C72351	hypothetical prote
19	82	8.2	595	2	JC6550	sex-determining re
20	82	8.2	649	2	T32668	hypothetical prote
21	81.5	8.2	446	2	C85343	hypothetical prote
22	81	8.1	237	2	S70797	vsaE1 protein - My
23	81	8.1	309	2	S70793	vsaE2 protein - My
24	81	8.1	314	2	F90577	lipoprotein vsaE [
25	80.5	8.1	808	2	C72858	AcOrf-66 protein -
26	80.5	8.1	821	2	T24728	hypothetical prote
27	80.5	8.1	1040	2	AH1926	hypothetical prote
28	80	8.0	1094	2	S22573	DNA-directed DNA p
29	80	8.0	1939	2	T18372	repeat organellar
30	79.5	8.0	214	2	JC5043	granulocyte colony
31	79.5	8.0	281	1	I40679	beta-hydroxybutyry
32	79.5	8.0	981	2	T18234	beta transducin ho
33	79	7.9	363	2	T22594	hypothetical prote
34	79	7.9	749	2	A96732	unknown protein F5
35	79	7.9	1214	2	JC7259	Smad interacting p
36	78.5	7.9	370	2	E64587	cag pathogenicity
37	78.5	7.9	1108	2	T06633	hypothetical prote
38	78	7.8	954	2	E86174	protein F19P19.26
39	78	7.8	1312	2	T30845	probable DNA repai
40	78	7.8	1902	2	C97702	cell surface antig
41	77.5	7.8	221	2	S39902	nwsB protein - Bra
42	77.5	7.8	271	2	AH1663	amino acid ABC tra
43	77.5	7.8	465	2	A84548	probable protein k
44	77	7.7	431	2	C88957	protein ZK697.2 [i
45	77	7.7	1091	2	A58532	glial cell membran

ALIGNMENTS

RESULT 1
B38957
interleukin 12A precursor [validated] - human
N;Alternate names: cytotoxic lymphocyte maturation factor 35K chain; natural killer c
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 01-Dec-2000
C;Accession: B38957; A39359; A36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric
A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: B38957
A;Molecule type: mRNA
A;Residues: 1-253 <WOL>
A;Cross-references: GB:M65290
A;Note: it is uncertain whether Met-1 or Met-35 is the initiator
R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nab
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactiv
A;Reference number: A39359; MUID:91239523; PMID:1674604
A;Accession: A39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 35-246,'T',248-253 <GUB>
A;Cross-references: GB:M65271; GB:M38443; NID:g180623; PIDN:AAA35694.1; PID:g180624
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lympho
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: A36055
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'X',58-70,'X',72-82 <STE>
C;Genetics:
A;Gene: GDB:IL12A; NKSF1
A;Cross-references: GDB:127869; OMIM:161560
A;Map position: 3p12-3q13.2
C;Keywords: cytokine; glycoprotein; heterodimer
F;57-253/Product: interleukin 12A #status predicted <MAT>
F;127,141,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.0%; Score 875; DB 2; Length 253;
Best Local Similarity 86.8%; Pred. No. 1.5e-69;
Matches 171; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

```
Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||| |||||||| | ||||||||||||||||||
Db         57 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 116

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||| ||||| ||| | |||||||||| | |||  ||||||||||||||:||| ||
```

```
Db        117 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 176

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||  ||||:|||||| ||||||||||||||||||||||||||||
Db        177 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 236

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        237 RIRAVTIDRVMSYLNAS 253


RESULT 2
I56135
interleukin 12 p35 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I56135
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.;
J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I56135
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: GB:M86672; NID:g198336; PIDN:AAA39292.1; PID:g198337

  Query Match            55.6%;  Score 553;  DB 2;  Length 215;
  Best Local Similarity  56.6%;  Pred. No. 2.5e-41;
  Matches  111;  Conservative   30;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          2 SLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVE 61
              ||    |  |  :||: |:|||:   : :: ||: |: ||||:|:|||||||:|:|||::
Db         20 SLARVIPVSGPARCLSQSRNLLKTTDDMVKTAREKLKHYSCTAEDIDHEDITRDQTSTLK 79

Qy         62 ACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNA 121
              ||||||  ||||||:|| |  | ||||   | | |  ||| ||||||||||| ||:|:||
Db         80 TCLPLELHKNESCLATRETSSTTRGSCLPPQKTSLMMTLCLGSIYEDLKMYQTEFQAINA 139

Qy        122 KLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFR 181
              |     :|| ||: || |||||:|:|| |  |: ||  : | | |: |:|||||||||
Db        140 ALQNHNHQQIILDKGMLVAIDELMQSLNHNGETLRQKPPVGEADPYRVKMKLCILLHAFS 199

Qy        182 IRAVTIDRMMSYLNSS 197
              | |||:|:| ||:|:
Db        200 TRVVTINRVMGYLSSA 215


RESULT 3
D84601
hypothetical protein At2g21450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D84601
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84601
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-816 <STO>
A;Cross-references: GB:AE002093; NID:g4567276; PIDN:AAD23689.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g21450
A;Map position: 2

  Query Match            9.8%;  Score 97.5;  DB 2;  Length 816;
  Best Local Similarity  23.2%;  Pred. No. 1.4;
  Matches   52;  Conservative   34;  Mismatches   79;  Indels   59;  Gaps    9;

Qy         20 QNLLRAVSNTLQKARQ-------TLELYS--CTSEEIDHEDITKDKTSTVEACL--PLEL 68
              || :  | | |   |         | |: |   :  ||         :|::|      :||
Db        442 QNNVEEVFNILDLVRPKFLKRPGTREIVSRIMSKAEIPRGKQVNQSSSSIEGTFFAAVEL 501

Qy         69 TMNESCLASREISLI--------------TNGSCLASGKASFMTVLCLSSIYED----- 108
              |:  |   | : |||                : | |  | : |  :| ||||  |
Db        502 TLQRSTNFSAKASLIKDLREMTRNILHYHKADFSGLLPGLSEFTVMLNLSSIQRDEVKGL 561

Qy        109 LKMYQMEFKAMNAKLLMDPKRQIFLDQN------------MLTAIDELLQALNFNSVTV 155
               ||   :  :: | | : || : ||::|              :  :|::|: :|     |
Db        562 RKMELFKQISLGAALYIHPKLKSFLEENPSNGEKGFSDNNTTVMKLDKMLKKINVRD-GV 620

Qy        156 PQKSSLEEPDFYKTKIKLC-------ILLHAFRIRAVTIDRMMS 192
                |       |:   : ||       ::   : :   |::|:||
Db        621 KMK-------FFLNLLALCESTGEKLLVFSQYIVPIKTLERLMS 657


RESULT 4
F97846
hypothetical protein RC1174 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: F97846
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: F97846
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1583 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL03712.1; PID:g15620302; GSPDB:GN00173
C;Genetics:
A;Gene: RC1174

  Query Match            9.4%;  Score 93;  DB 2;  Length 1583;
  Best Local Similarity  22.6%;  Pred. No. 8.2;
  Matches   47;  Conservative   40;  Mismatches   71;  Indels   50;  Gaps    9;

Qy          9 SPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLEL 68
              | |:  | :|  |:  |:|: :   : |||          :   :  | |  ||     ||
Db       1140 SAGV-DCSDHEVNIKIALSSAITSGKITLE---------ERNKLLNDMTKQVE-----EL 1184

Qy         69 TMNESCLASREISLITNGSCLASGKASFMTVLCLS---SIYEDLKMYQME---------- 115
                : ::   :  |:::     |        ||  ||    | |: |: : |
Db       1185 VLIDNYKQTEAITIMQLSPTL--------TVNILSQFIDILEEEKVLERENEFLPSAEEL 1236

Qy        116 -FKAMNAKLLMDPKRQIFLDQNMLTAIDELLQAL-----NFNSVTVPQKSSLEEPDFYKT 169
               :||: ::|  |:  | |  :  :|  ||: :       |::  :        |:  :
Db       1237 NSRAMSGEVLTRPELCILLSYSKRSAYHELINSTFSHDKYFDAYLIDY-----FPEMMQK 1291

Qy        170 KIKLCILLHAFR---IRAVTIDRMMSYL 194
              | :  || |  :   |: |||:::|: |
Db       1292 KFRNEILSHPLKHEIIKTVTINKIMNQL 1319


RESULT 5
T20187
hypothetical protein C53D6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20187
R;Gardner, A.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19235
A;Accession: T20187
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-615 <WIL>
A;Cross-references: EMBL:Z70270; PIDN:CAA94225.1; GSPDB:GN00022; CESP:C53D6.6
A;Experimental source: clone C53D6
C;Genetics:
A;Gene: CESP:C53D6.6
```

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A;Map position: 4
A;Introns: 44/1; 387/3; 447/3; 528/3

  Query Match             9.1%;  Score 90;  DB 2;  Length 615;
  Best Local Similarity   25.1%;  Pred. No. 4.6;
  Matches   43;  Conservative   30;  Mismatches   62;  Indels   36;  Gaps    9;

Qy         26 VSNTLQKARQTLE--LYSCTSEEIDHEDIT-----KDKTSTVEACLPLELTMNESCLASR 78
              ||| |: : | ||  :| ||    :    |:         |  :| |  :   :||| :
Db        251 VSN-LKLSAQLLEFDIYDCTWNSLSLASISGINTIPGGTELIEKCKKIVQKINESAVYET 309

Qy         79 ----EISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLD 134
                  |   | :   : ||| :::||:   |::|       : | :    ||:    : |
Db        310 SLIGEYMTIDSADLVKSGKLNWITVV---SMFEQF----TKLKGLLDTFLMNDMEGLMLY 362

Qy        135 QNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAV 185
              |     :: :|: |:      | |:::   || |         | ||| |:
Db        363 QQDYDLMEIILRTLS------PLKTAV---DFGKQ--------HTFRISAI 396


RESULT 6
F71550
probable endonuclease CT154 [similarity] - Chlamydia trachomatis (serotype D, strain UW3
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 04-Feb-2000
C;Accession: F71550
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: F71550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-383 <ARN>
A;Cross-references: GB:AE001289; GB:AE001273; NID:g3328550; PIDN:AAC67745.1; PID:g332855
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: CT154

  Query Match             8.9%;  Score 88.5;  DB 2;  Length 383;
  Best Local Similarity   27.8%;  Pred. No. 3.5;
  Matches   32;  Conservative   23;  Mismatches   53;  Indels    7;  Gaps    3;

Qy          4 PTASPSPGIFQCLNHSQ--NLLRAVSNTLQKARQ--TLELYSCTSEEIDHEDITKDKTST 59
              | |     ||  ::  |  | || : :|:::|::   : :|: :|::|    |
Db         50 PLAERELIIFHSVHQQQNNNPLRMICDTIRQAQRGIFMRIYTISSDDIIQSLIQTSHHVP 109

Qy         60 VEACLPLELTMNESCLASREISLITNGSCLASGK---ASFMTVLCLSSIYEDLKM 111
              ||      ::  :|  || :  :|||  |   |   | | ||:  |: | || :
Db        110 VEVKYHCGESLPVACQNSRVVLRLTNGRTLQHKKTMLADFQTVVTGSANYTDLSL 164


RESULT 7
S53955
hypothetical protein YML117w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8339.02
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S53955
R;Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S53954
A;Accession: S53955
A;Molecule type: DNA
A;Residues: 1-1134 <SKE>
A;Cross-references: EMBL:Z49210; NID:g798881; PIDN:CAA89101.1; PID:g798883; GSPDB:GN0001
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YML117w
A;Cross-references: SGD:S0004585
A;Map position: 13L

  Query Match             8.7%;  Score 86.5;  DB 2;  Length 1134;
  Best Local Similarity   24.8%;  Pred. No. 20;
  Matches   50;  Conservative   27;  Mismatches   54;  Indels   71;  Gaps   12;

Qy         15 CLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDH----EDITKD--KTSTVEACLPLE- 67
              |:|:       |  |   | :|  |     | :||      | |:  |::|:|:   :|
Db        198 CINYK------VLPTGDDAYRTRSL---LIENVDHSIDLHSIVKNFVKSNTLESAYLIEG 248

Qy         68 ---------LTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFK- 117
                      | | | |    || :| | ||               : | ::     |||
Db        249 GKSDDSKDVETKNLSIL----ISFLTKGDCL--------------NFYNNILQRLSEFKT 290

Qy        118 -----AMNAK---LLMDPK-RQIFLDQNMLTAIDE----------LLQALNFN------- 151
                  |:| |   |  |||    |::   ||   |           :  :|: |
Db        291 FLKSEALNLKFVCLNYDPKCLPTFIESEALTENAEEADITNGSTMISASLHHNIANKDAT 350

Qy        152 -SVTVPQKSSLEEPDFYKTKIK 172
               |: :  || :|: | :| |::
Db        351 RSIIIEFKSPVEKSDLFKKKLQ 372


RESULT 8
T16507
hypothetical protein F59A6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16507
R;Nhan, M.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F59A6.
A;Reference number: Z18526
A;Accession: T16507
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1286 <NHA>
A;Cross-references: EMBL:U41994; NID:g1123047; PID:g1123050; PIDN:AAA83454.1; CESP:F5
C;Genetics:
A;Gene: CESP:F59A6.5
A;Introns: 35/3; 335/3; 685/3; 973/3; 1097/3

  Query Match             8.7%;  Score 86;  DB 2;  Length 1286;
  Best Local Similarity   23.8%;  Pred. No. 26;
  Matches   41;  Conservative   28;  Mismatches   71;  Indels   32;  Gaps    6;

Qy         16 LNHSQNLLRAVSN---TLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNE 72
              | | |: :| : |    ||:  :|||:       | |       | :| |       || : :
Db        109 LKHHQSQIRILQNKCSTLEMEKQTLQ------ETIQRAQDDKKETET-----ELESSRSR 157

Qy         73 SCLASREISLITN------------GSCLASGKASFMTVLC-----LSSIYEDLKMYQME 115
                 :  :|:|   |                | | :  ::| |        :: | |: |: :
Db        158 LHVLEKELSAKANDIFMVTKDLHDKNEELTSFRMEYVTKLSEANREKKALEEKLEKYKND 217

Qy        116 FKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFY 167
              |  : | |   | |:   ||:|: : :|     | :      | : | | |
Db        218 MKENDRKSLELNKEQV-TTQNVLSEVRQLSAHFEFLTPVRKNASKIRELDEY 268


RESULT 9
T38077
hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38077
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z21767
A;Accession: T38077
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1957 <CON>
A;Cross-references: EMBL:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
A;Experimental source: strain 972h-; cosmid c1F3
C;Genetics:
A;Gene: SPDB:SPAC1F3.06c
```

```
A;Map position: 1

  Query Match             8.6%;  Score 85.5;  DB 2;  Length 1957;
  Best Local Similarity   20.4%;  Pred. No. 49;
  Matches   46;  Conservative   47;  Mismatches   78;  Indels   55;  Gaps    8;

Qy          3 LPTASPSPGIFQCL-NHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHE---------- 50
              | :|    |  | | : | :|:  : : ||:|:: ::::   | :|:|||
Db       1476 LASAVEKLGALQKLHSESLSLMENIKSQLQEAKEKIQVDESTIQELDHEITASKNNYEGK 1535

Qy         51 -----DITKDKTSTVEA---CLPLELTMNESCLASREISLITNGSCLAS---------- 91
                 | :| :  :|     |  | :  :     :|  ::   | ||
Db       1536 LNDKDSIIRDLSENIEQLNNLLAEEKSAVKRLSTEKESEILQFNSRLADLEYHKSQVESE 1595

Qy         92 -GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNF 150
               |::     | |:|  |:|:: : |  ::  ::| | : |:    |:  :: | |: |
Db       1596 LGRSK----LKLASTTEELQLAENERLSLTTRML-DLQNQVKDLSNIKDSLSEDLRTLR- 1649

Qy        151 NSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNS 196
                 |||:         :  |    :|:: |:: :   | |
Db       1650 ---------SLED--------SVASLQKECKIKSNTVESLQDVLTS 1678


RESULT 10
A41185
alpha-2 macroglobulin MUG1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 12-Apr-1995
C;Accession: A41185
R;Overbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
J. Biol. Chem. 266, 16903-16910, 1991
A;Title: Molecular characterization of the murinoglobulins.
A;Reference number: A41185; MUID:91358495; PMID:1840592
A;Accession: A41185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1476 <OVE>
A;Cross-references: GB:M65736
C;Superfamily: alpha-2-macroglobulin

  Query Match             8.6%;  Score 85;  DB 2;  Length 1476;
  Best Local Similarity   24.2%;  Pred. No. 38;
  Matches   38;  Conservative   30;  Mismatches   47;  Indels   42;  Gaps    8;

Qy         74 CLASREISLITNGSCLASGKASFMTVLCLSSIYED------LKMYQM-EFKAMNAKLLMD 126
              || |  :: : : | | :| : :| ||  | :| :      | :||: |   : | |:
Db         10 CLFSVLLAFLHSAS-LLNGDSKYM-VLVPSQLYTETPEKICLHLYQLNETVTVTASLVSQ 67

Qy        127 PKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIK---------LCILL 177
                |:   |: :|    :| | ::|    :|: || :| ||    ||          :|:
Db         68 SGRKNLFDELVLD--KDLFQCVSF---IIPRLSSSDEEDFLYVDIKGPTHEFSKRKAVLV 122

Qy        178 ------------------HAFRIRAVTIDRMMSYLN 195
                             : : | |::|:|:  ||
Db        123 KNKESVVFVQTDKPVYKPGQSVKFRVVSMDKMLRPLN 159


RESULT 11
T33611
hypothetical protein F54D10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33611
R;Sammons, L.; Wohldmann, P.; Clarke, K.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid F54D10.
A;Reference number: Z21377
A;Accession: T33611
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-310 <SAM>
A;Cross-references: EMBL:AF099917; PIDN:AAC68781.1; GSPDB:GN00020; CESP:F54D10.3
A;Experimental source: strain Bristol N2; clone F54D10
C;Genetics:
A;Gene: CESP:F54D10.3
A;Map position: 2
A;Introns: 162/2; 234/3

  Query Match             8.5%;  Score 84.5;  DB 2;  Length 310;
  Best Local Similarity   22.0%;  Pred. No. 6;
  Matches   40;  Conservative   41;  Mismatches   54;  Indels   47;  Gaps   10;

Qy         21 NLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREI 80
              ||:: |   : : ::  :|:: ::::|| |     :  ||     :||      | |  :
Db         22 NLIKKVFLNILEPKE--DLWN-SNQKIDRE-----RWETV----GIELFQRTGILVS--V 67

Qy         81 SLITNG-------------SCLASGKASFMTVLCLS--SIYEDLKMYQMEF--------- 116
                 : :|             :|: || :   | | |    :::||: |  :
Db         68 DQMRSGFRSIKSNLGQRLHNCVQSGMSRIQTELELQKWELFQDLRFYYDKLYKYRQLRAE 127

Qy        117 ----KAMNAKLLMDPKRQIFLDQ-NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKI 171
                  :| |:: :      | | :: :|:: ::|   |: : |  :|| ||   |    ||:
Db        128 RTGNEARNSEPVSGEDMQSFFEEPDMMSLVEENDSAMKYLSSLIPQVSSTSTP----TKV 183

Qy        172 KL 173
              ||
Db        184 KL 185


RESULT 12
C97303
hypothetical protein CAC3280 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C97303
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97303
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-849 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81214.1; PID:g15026357; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3280

  Query Match             8.5%;  Score 84;  DB 2;  Length 849;
  Best Local Similarity   25.7%;  Pred. No. 23;
  Matches   45;  Conservative   30;  Mismatches   70;  Indels   30;  Gaps    8;

Qy         16 LNHSQNLLRAVSN-TLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESC 74
              || : | :  :|: |  |  ||| | | | ::|   |: |: |      |      : |
Db        669 LNLNSNKINDISSLTNLKQLQTLSLNSNTIQDI---DVLKNFTVLNVLGLSNNKITDIST 725

Qy         75 LAS----REISL----ITNGSCLAS-GKASFM--------TVLCLSSIYEDLKMY--QME 115
              ||:    : |||    ||| ||| :   | ::          :  |: :     :|   :
Db        726 LANLNSLKNISLSNNQITNISCLCNLTNAQYLHLENNQINDISALNKLKNLAYLYLNNNQ 785

Qy        116 FKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNF-------NSVTVPQKSSLEE 163
                 : |   :|    ::|  | :| :| | |    |        |::|   ::||:|
Db        786 ITDITALGFLDKLNTLYLSYNKITKVDSLKNLTNLKILILAENNITSTDQTSLKE 840


RESULT 13
JC7116
Xsal-3 protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7116
R;Onuma, Y.; Nishinakamura, R.; Takahashi, S.; Yokota, T.; Asashima, M.
Biochem. Biophys. Res. Commun. 264, 151-156, 1999
A;Title: Molecular cloning of a novel Xenopus spalt gene (Xsal-3).
A;Reference number: JC7116; MUID:99458636; PMID:10527856
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```
A;Accession: JC7116
A;Molecule type: DNA
A;Residues: 1-1061 <ONU>
A;Cross-references: DDBJ:AB030827
A;Experimental source: egg, neural tube
C;Genetics:
A;Gene: Xsal-3
C;Keywords: egg; zinc finger

  Query Match             8.4%;  Score 83;  DB 2;  Length 1061;
  Best Local Similarity   27.0%;  Pred. No. 38;
  Matches   43;  Conservative   19;  Mismatches   57;  Indels   40;  Gaps    8;

Qy         19 SQNLLRAVSNTLQKA-RQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS 77
              || |  ||:   ||| |:| | |    :: | ::      ||    || ||   : |
Db        238 SQQLSAAVALIGQKAGTQSLSLESLKQSKLPHSNVAMPTAGTV----PLALT---TSLLK 290

Qy         78 REISL-ITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQN 136
              :| :| :||    | |:                        |  |   |   ||  ||
Db        291 QEPNLGLTN----AVGRFP-----------------------NPALPHSPGTIIF--QN 320

Qy        137 MLTAIDELLQ-ALNFNSVTVPQKSSLEEPDFYKTKIKLC 174
              : |:|   :  : | :|| |:     |   :: | | |
Db        321 PINALDPSKKLKVKFPTVTTPEAKPGNEDQLFRHKCKFC 359


RESULT 14
AB1292
amino acid ABC transporter (binding protein) homolog lmo1738 [imported] - Listeria monoc
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AB1292
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1292
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99816.1; PID:g16411192; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1738
C;Superfamily: lysine-arginine-ornithine-binding protein

  Query Match             8.3%;  Score 82.5;  DB 2;  Length 271;
  Best Local Similarity   25.6%;  Pred. No. 7.6;
  Matches   34;  Conservative   18;  Mismatches   60;  Indels   21;  Gaps    3;

Qy         65 PLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLL 124
              |:: || || | :  | || ||  :   :      :  |  |   :   :  |: |
Db         82 PIDWTMKESELKNGSIDLIWNGYTVTDARKK---QVAFSQPYMKNEQVLVTLKSSNINQF 138

Qy        125 MDPKRQIFLDQNMLTAIDE-------LLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILL 177
               | | :    ||  ::||:       |   :| |          ||: | |     | |
Db        139 SDMKNKTLGAQNGASSIDDMAKKPEVLTDIINNN----------EPELYDTFDTAFIDL 187

Qy        178 HAFRIRAVTIDRM 190
              :  ||  : || :
Db        188 NNKRIDGLIIDEV 200


RESULT 15
D86492
hypothetical protein CPj0012 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: D86492
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: D86492
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-523 <STO>
A;Cross-references: GB:BA000008; NID:g8978385; PIDN:BAA98222.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0012

  Query Match             8.3%;  Score 82.5;  DB 2;  Length 523;
  Best Local Similarity   18.6%;  Pred. No. 17;
  Matches   41;  Conservative   40;  Mismatches   79;  Indels   61;  Gaps    7;

Qy         16 LNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCL 75
              |  |: :|      :: |  ::  ::   |  | :   |     : : || |:   |:||
Db        253 LKKSKTMLDRAKWHIENAEDSITWWTSQIEMKDMKARLKILKEDITSVLP-EIDEIETCL 311

Qy         76 ASREISLITNGSCLASGKASFM----TVLCLSSIYED---LKMYQMEFKAMNAKL----- 123
              :  |: |:|    |      |     |:| ::|::|:   :: |::: : :  ||
Db        312 SLEELPLLTTRELLTKSYLKFKICSETLLKMTSVFENNIYVQEYEVQLQNLGFKLQGISQ 371

Qy        124 --------LMDPKRQIFLDQNMLTAIDELLQALNFNSV---------------TVPQKSS 160
                     : : |: | :  |  : :  :   || :                 |  || :
Db        372 RFGKKQDDFANLEEQVALQKKRLRELTQNFEIQGFNFMKEDFKAAAKDLYIRSTAEQKMN 431

Qy        161 LEEP-----------------------DFYK-TKIKLCIL 176
               : |                      | |:  | ||| |
Db        432 FDVPCMELFRRYHEEVNKPLLELMYNCADSYRDAKKKLCSL 472


Search completed: July 15, 2003, 11:08:41
Job time : 9.63459 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:28 ; Search time 4.31729 Seconds
(without alignments)
1892.583 Million cell updates/sec

Title: US-09-917-265-50
Perfect score: 994
Sequence: 1 RSLPTASPSPGIFQCLNHSQ.....HAFRIRAVTIDRMMSYLNSS 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	973	97.9	222	1	I12A_CANFA	Q28267 canis famil
2	929	93.5	222	1	I12A_FELCA	O02743 felis silve
3	876	88.1	222	1	I12A_PIG	Q29053 sus scrofa
4	875	88.0	219	1	I12A_HUMAN	P29459 homo sapien
5	858	86.3	222	1	I12A_HORSE	Q9xsq6 equus cabal
6	838.5	84.4	221	1	I12A_CEREL	Q28233 cervus elap
7	835.5	84.1	221	1	I12A_SHEEP	Q9tu27 ovis aries
8	833.5	83.9	221	1	I12A_BOVIN	P54349 bos taurus
9	829	83.4	219	1	I12A_MACMU	P48091 macaca mula
10	824	82.9	219	1	I12A_CERTO	P46661 cercocebus
11	818.5	82.3	221	1	I12A_CAPHI	O02814 capra hircu
12	592.5	59.6	223	1	I12A_MARMO	Q61728 marmota mon
13	553	55.6	215	1	I12A_MOUSE	P43431 mus musculu
14	86.5	8.7	1134	1	YML7_YEAST	Q03735 saccharomyc
15	85.5	8.6	1957	1	YD86_SCHPO	Q10411 schizosacch
16	85	8.6	1476	1	A2M1_MOUSE	P28665 mus musculu
17	84.5	8.5	3210	1	CENF_HUMAN	P49454 homo sapien
18	84	8.5	734	1	G13B_DICDI	P34116 dictyosteli
19	82	8.2	984	1	SX13_MOUSE	Q04891 mus musculu
20	80.5	8.1	355	1	GBAC_CAEEL	Q19572 caenorhabdi
21	80.5	8.1	808	1	Y066_NPVAC	P41467 autographa
22	80.5	8.1	821	1	LIN5_CAEEL	P45970 caenorhabdi
23	80	8.0	1094	1	DPOD_PLAFK	P30315 plasmodium
24	79.5	8.0	281	1	HBD_CLODI	P45364 clostridium
25	77	7.7	1018	1	ST31_MOUSE	Q99mw1 mus musculu
26	77	7.7	1351	1	RPOM_YEAST	P13433 saccharomyc
27	76.5	7.7	1170	1	SMC2_YEAST	P38989 saccharomyc
28	76	7.6	583	1	LAM1_XENLA	P09010 xenopus lae
29	76	7.6	970	1	PSU1_YEAST	P53550 saccharomyc
30	76	7.6	1243	1	DPOA_ORYSA	O48653 oryza sativ
31	75.5	7.6	561	1	SR72_SCHPO	O59787 schizosacch
32	75.5	7.6	1581	1	AROL_PNECA	Q12659 p pentafunc
33	75.5	7.6	2504	1	FAS_HUMAN	P49327 homo sapien
34	75	7.5	701	1	HS83_LEIIN	Q25293 leishmania
35	74.5	7.5	565	1	ESR3_MICUN	P57783 micropogoni
36	74.5	7.5	2871	1	DESP_HUMAN	P15924 homo sapien
37	74	7.4	409	1	GCDH_CAEEL	Q20772 caenorhabdi
38	74	7.4	429	1	FLIK_BACSU	P23451 bacillus su
39	74	7.4	2505	1	FAS_RAT	P12785 rattus norv
40	73.5	7.4	571	1	SYQ_BUCAI	P57490 buchnera ap
41	73.5	7.4	979	1	P115_MYCHR	P41508 mycoplasma
42	73.5	7.4	2569	1	LMA3_MOUSE	Q61789 mus musculu
43	73.5	7.4	3433	1	UTRO_HUMAN	P46939 homo sapien
44	73	7.3	273	1	OSA6_BORBU	Q09088 borrelia bu
45	73	7.3	448	1	FDFT_CANAL	P78589 candida alb

ALIGNMENTS

RESULT 1
I12A_CANFA
ID I12A_CANFA STANDARD; PRT; 222 AA.
AC Q28267;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE maturation factor 35 kDa subunit) (CLMF p35).
GN IL12A.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98280561; PubMed=9617567;
RA Buettner M., Belke-Louis G.F., Rziha H.J., McInnes C., Kaaden O.R.;
RT "Detection, cDNA cloning and sequencing of canine interleukin 12.";
RL Cytokine 10:241-248(1998).
CC -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC BY RESTING PBMC (BY SIMILARITY).
CC -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC ----------
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC ----------
DR EMBL; U49085; AAA92058.1; -.
DR InterPro; IPR004281; IL12.
DR Pfam; PF03039; IL12; 1.
KW Cytokine; Growth factor; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 222 INTERLEUKIN-12 ALPHA CHAIN.
FT DISULFID 99 99 INTERCHAIN (PROBABLE).
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 222 AA; 24992 MW; 48C7E53ECFD6ACE5 CRC64;

Query Match 97.9%; Score 973; DB 1; Length 222;
Best Local Similarity 98.0%; Pred. No. 2.7e-79;
Matches 193; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
Db 26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTV 85

```
Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 2
I12A_FELCA
ID   I12A_FELCA     STANDARD;      PRT;   222 AA.
AC   O02743; O46672;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97246745; PubMed=9089110;
RA   Schijns V.E.C.J., Wierda C.M.H., Vahlenkamp T.W., Horzinek M.C.;
RT   "Molecular cloning of cat interleukin-12.";
RL   Immunogenetics 45:462-463(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98182592; PubMed=9522125;
RA   Fehr D., Dean G.A., Huder J., Fan Z., Huettner S., Higgins J.W.,
RA   Pedersen N.C., Lutz H.;
RT   "Nucleotide and predicted peptide sequence of feline interleukin-12
RT   (IL-12).";
RL   DNA Seq. 8:77-82(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y07761; CAA69067.1; -.
DR   EMBL; U83185; AAB93836.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    183    183       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     66     66       S -> P (IN REF. 2).
FT   CONFLICT    221    221       A -> S (IN REF. 2).
SQ   SEQUENCE   222 AA;  25076 MW;  223CF8FE0D30BF17 CRC64;

  Query Match             93.5%;  Score 929;  DB 1;  Length 222;
  Best Local Similarity   92.4%;  Pred. No. 2.1e-75;
  Matches  182;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db         26 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||||||||||||||||||||||||| | |||| |||||||||||||:||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:|||||||:|
Db        206 RIRAVTINRMMSYLNAS 222


RESULT 3
I12A_PIG
ID   I12A_PIG       STANDARD;      PRT;   222 AA.
AC   Q29053;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97383978; PubMed=9239844;
RA   Foss D.L., Murtaugh M.P.;
RT   "Molecular cloning and mRNA expression of porcine interleukin-12.";
RL   Vet. Immunol. Immunopathol. 57:121-134(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L35765; AAA73897.1; ALT_INIT.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   222 AA;  24945 MW;  027D04411333AC94 CRC64;
```

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  Query Match             88.1%;  Score 876;  DB 1;  Length 222;
  Best Local Similarity   86.8%;  Pred. No. 1.1e-70;
  Matches  171;  Conservative   10;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||  :  ||:|:|||||||||:|||||||||:|||| |||||||||||||||||||||
Db         26 RSLPATTAGPGMFKCLNHSQNLLKAVSNTLQKAKQTLEFYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||| |||||||:|| ||||||:|| ||| |||| |||||||||||||| :||:|||
Db         86 EACLPLELATNESCLAARETSLITNGNCLTSGKTSFMTTLCLSSIYEDLKMYHVEFQAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||| ||:||||||| ||||| |||| |||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAITELMQALNFNSETVPQKPSLEELDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 4
I12A_HUMAN
ID   I12A_HUMAN     STANDARD;      PRT;   219 AA.
AC   P29459; Q96QZ1;
DT   01-APR-1993 (Rel. 25, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35) (NK cell stimulatory
DE   factor chain 1) (NKSF1).
GN   IL12A OR NKSF1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91239523; PubMed=1674604;
RA   Gubler U., Chua A.O., Schoenhaut D.S., Dwyer C.M., McComas W.,
RA   Motyka R., Nabavi N., Wolitzky A.G., Quinn P.M., Familletti P.C.,
RA   Gately M.K.;
RT   "Coexpression of two distinct genes is required to generate secreted
RT   bioactive cytotoxic lymphocyte maturation factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4143-4147(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91201875; PubMed=1673147;
RA   Wolf S.F., Temple P.A., Kobayashi M., Young D., Dicig M., Lowe L.,
RA   Dzialo R., Fitz L., Ferenz C., Hewick R.M., Kelleher K.,
RA   Herrmann S.H., Clark S.C., Azzoni L., Chan S.H., Trinchieri G.,
RA   Perussia B.;
RT   "Cloning of cDNA for natural killer cell stimulatory factor, a
RT   heterodimeric cytokine with multiple biologic effects on T and
RT   natural killer cells.";
RL   J. Immunol. 146:3074-3081(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 23-48.
RX   MEDLINE=90370873; PubMed=2204066;
RA   Stern A.S., Podlaski F.J., Hulmes J.D., Pan Y.C.E., Quinn P.M.,
RA   Wolitzky A.G., Familletti P.C., Stremlo D.L., Truitt T.,
RA   Chizzonite R., Gately M.K.;
RT   "Purification to homogeneity and partial characterization of
RT   cytotoxic lymphocyte maturation factor from human B-lymphoblastoid
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6808-6812(1990).
RN   [5]
RP   SIMILARITY TO IL-6.
RX   MEDLINE=92247293; PubMed=1374259;
RA   Merberg D.M., Wolf S.F., Clark S.C.;
RT   "Sequence similarity between NKSF and the IL-6/G-CSF family.";
RL   Immunol. Today 13:77-78(1992).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
CC       T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC.
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS. NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE
CC       RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M65271; AAA35694.1; -.
DR   EMBL; M65291; AAA59937.1; ALT_INIT.
DR   EMBL; AF404773; AAK84425.1; -.
DR   PIR; A39359; A39359.
DR   PIR; A36055; A36055.
DR   Genew; HGNC:5969; IL12A.
DR   MIM; 161560; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     22
FT   CHAIN       23    219       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     96     96       INTERCHAIN (PROBABLE).
FT   CARBOHYD     93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    213    213       M -> T (IN REF. 1).
SQ   SEQUENCE   219 AA;  24874 MW;  7C658AB7716112B2 CRC64;

  Query Match             88.0%;  Score 875;  DB 1;  Length 219;
  Best Local Similarity   86.8%;  Pred. No. 1.3e-70;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| ||||||||| | ||||||||||||||||||
Db         23 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||| ||||| ||| | ||||||||| | |||  |||||||||||||:||| ||
Db         83 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 142

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        143 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        203 RIRAVTIDRVMSYLNAS 219


RESULT 5
I12A_HORSE
ID   I12A_HORSE     STANDARD;      PRT;   222 AA.
AC   Q9XSQ6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20009534; PubMed=10541814;
RA   Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA   Argyle D.J., Onions D.E.;
RT   "Cloning and sequencing of horse interleukin-12 and interleukin-18
RT   cDNAs.";
RL   Immunogenetics 50:94-97(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y11130; CAA72012.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD    42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   222 AA;  24800 MW;  5AD6DA874CE7AD2A CRC64;

  Query Match             86.3%;  Score 858;  DB 1;  Length 222;
  Best Local Similarity   84.8%;  Pred. No. 4.2e-69;
  Matches  167;  Conservative   13;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||||:| ||:|||||||||||| |||||||||||| |||||||||||||||||:|||
Db         26 RNLPTATPGPGMFQCLNHSQNLLRTVSNTLQKARQTLEFYSCTSEEIDHEDITKDKSSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
               |||||||  |||||||||| ||||||| |||| | |||||||||||||:||||||
Db         86 AACLPLELAPNESCLASREISFITNGSCLTPGKASSMMTLCLSSIYEDLKMYQVEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||:||:|||||:|||||||:|:||||||| ||||| ||| |||||:|||||||||
Db        146 AKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETVPQKPSLEGLDFYKTKVKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:||| |||:|
Db        206 RIRAVTINRMMGYLNAS 222


RESULT 6
I12A_CEREL
ID   I12A_CEREL     STANDARD;      PRT;   221 AA.
AC   Q28233;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99304506; PubMed=10376218;
RA   Lockhart E., Slobbe L., Buchan G.;
RT   "The characterisation of a cervine immunoregulatory cytokine,
RT   interleukin 12.";
RL   DNA Seq. 10:139-148(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U57751; AAB02257.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    221       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD    41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   221 AA;  24899 MW;  5125E84A53C388DC CRC64;

  Query Match             84.4%;  Score 838.5;  DB 1;  Length 221;
  Best Local Similarity   85.3%;  Pred. No. 2.2e-67;
  Matches  168;  Conservative    8;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              ||||  :  ||   |||:|||||||:|||||||||| ||||||||||||||||||||
Db         26 RSLPPTTAGPG-RSCLNYSQNLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 84

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||  ||||| ||| ||||:|||||||| |||| ||| |||||||| |||:|||
Db         85 EACLPLELATNESCLVSRETSLITHGSCLASGKTSFMTTLCLKSIYEDLKMYHMEFQAMN 144

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||| || ||:|||||| ||||| |||| |||||||:|||||||||
Db        145 AKLLMDPKRQIFLDQNMLAAIAELMQALNFNSETVPQKPSLEEMDFYKTKVKLCILLHAF 204

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||:||
Db        205 RIRAVTIDRMMSYLSSS 221


RESULT 7
I12A_SHEEP
ID   I12A_SHEEP     STANDARD;      PRT;   221 AA.
AC   Q9TU27; Q9MYU0;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A OR IL12P35.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
```

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RN   [1]
RP   SEQUENCE FROM N.A., AND SUBUNIT.
RC   TISSUE=Kidney;
RX   MEDLINE=20480126; PubMed=11023671;
RA   Swinburne S.J., Russ G.R., Krishnan R.;
RT   "Ovine interleukin 12 has biological activity on ovine and human
RT   activated peripheral blood mononuclear cells.";
RL   Cytokine 12:1546-1552(2000).
RN   [2]
RP   SEQUENCE OF 72-132 FROM N.A.
RX   MEDLINE=20539119; PubMed=11086544;
RA   Schmidt P., Kuehn C., Kang'a S., Hanotte O., Vanselow J., Anton I.,
RA   Langner C., Schwerin M.;
RT   "Interleukin-12 p35 encoding gene of cattle and sheep harbours a
RT   polymorphic T stretch in intron 4.";
RL   Anim. Genet. 31:283-285(2000).
CC   -!- FUNCTION: Cytokine that can act as a growth factor for activated T
CC       and NK cells, enhance the lytic activity of NK/lymphokine-
CC       activated Killer cells, and stimulate the production of IFN-gamma
CC       by resting PBMC (By similarity).
CC   -!- SUBUNIT: Disulfide-bonded heterodimer of 40 kDa and 35 kDa
CC       subunits.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF173557; AAD51976.1; -.
DR   EMBL; AJ271035; CAB97178.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal; Glycoprotein.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    221       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD    95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   221 AA;  24859 MW;  9E9A2300914E4167 CRC64;

  Query Match             84.1%;  Score 835.5;  DB 1;  Length 221;
  Best Local Similarity   84.3%;  Pred. No. 4.1e-67;
  Matches  166;  Conservative   11;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |||||  :  ||   ||::||||||||||||||||||| ||||||||||||||||||||
Db         26 RSLPTTTAGPGT-SCLDYSQNLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 84

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||  |||||||||| |||||| ||:||| |||| ||| |||:||||| |||:|||
Db         85 EACLPLELATNESCLASRETSLITNGHCLSSGKTSFMTTLCLRSIYKDLKMYHMEFQAMN 144

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||:|||||| || ||:|||||:| ||||| |||| |||||||:|||||||||
Db        145 AKLLMDPKRQVFLDQNMLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAF 204

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||:||
Db        205 RIRAVTIDRMMSYLSSS 221


RESULT 8
I12A_BOVIN
ID   I12A_BOVIN     STANDARD;      PRT;   221 AA.
AC   P54349;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Holstein; TISSUE=Lymphoid;
RX   MEDLINE=95244628; PubMed=7727547;
RA   Zarlenga D.S., Canals A., Aschenbrenner R.A., Gasbarre L.C.;
RT   "Enzymatic amplification and molecular cloning of cDNA encoding the
RT   small and large subunits of bovine interleukin 12.";
RL   Biochim. Biophys. Acta 1270:215-217(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U14416; AAA85810.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    221       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD    95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   221 AA;  24944 MW;  0462DEE9DD33BC90 CRC64;

  Query Match             83.9%;  Score 833.5;  DB 1;  Length 221;
  Best Local Similarity   84.8%;  Pred. No. 6.2e-67;
  Matches  167;  Conservative   10;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |||||  :  |||   ||::||||||||||||||||||| ||||||||||||||||||||
Db         26 RSLPTTTASPG-RSCLDYSQNLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 84

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||  |||||||||| | |||| |||||| |||| ||| |||||||||| :||:|||
Db         85 EACLPLELATNESCLASRETSFITNGHCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMN 144

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||| || ||:|||||:| ||||| ||:| |||||||:|||||||||
Db        145 AKLLMDPKRQIFLDQNMLAAIAELMQALNFDSETVPQKPSLKELDFYKTKVKLCILLHAF 204

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||:||
Db        205 RIRAVTIDRMMSYLSSS 221


RESULT 9
I12A_MACMU
ID   I12A_MACMU     STANDARD;      PRT;   219 AA.
AC   P48091;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
```

```
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U19842; AAA86707.1; ALT_INIT.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    219       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    96     96       INTERCHAIN (PROBABLE).
FT   CARBOHYD    24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   219 AA;  24904 MW;  D676D8B6663C4A33 CRC64;

  Query Match             83.4%;  Score 829;  DB 1;  Length 219;
  Best Local Similarity   82.7%;  Pred. No. 1.5e-66;
  Matches  163;  Conservative   10;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|  |:| | :| ||:||||||:| |||||||| || | ||||||||||||||||||
Db         23 RNLSVATPGPEMFPCLHHSQNLLKAASNTLQKARQILEFYPCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||| |||| ||| | ||||||||| | ||| ||| ||||||||||:||| ||
Db         83 EACLPLELIKNESCLNSRETSFITNGSCLASRKTSFMMALCLRSIYEDLKMYQVEFKTMN 142

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||| ||||||||||:|  ||||:||||||| ||||||||||||||||||||||||||
Db        143 AKLLRDPKRQIFLDQNILGVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        203 RIRAVTIDRVMSYLNAS 219


RESULT 10
I12A_CERTO
ID   I12A_CERTO     STANDARD;      PRT;   219 AA.
AC   P46661;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
```

```
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U19835; AAA86702.1; ALT_INIT.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    219       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    96     96       INTERCHAIN (PROBABLE).
FT   CARBOHYD    24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   219 AA;  24801 MW;  844770181AC771BF CRC64;

  Query Match             82.9%;  Score 824;  DB 1;  Length 219;
  Best Local Similarity   81.7%;  Pred. No. 4.2e-66;
  Matches  161;  Conservative   13;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|  |:| | :| ||:||||||:|  |||||||| || | ||||||||||||||||||
Db         23 RNLSVATPGPEMFPCLHHSQNLLKAACNTLQKARQILEFYPCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||  ||||| ||| | |:|||||||| | |||  ||| ||||||||:||:||| ||
Db         83 EACLPLELIKNESCLNSRETSVITNGSCLASRKTSFMMALCLRSIYEDLKIYQVEFKTMN 142

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||:|  ||||:||||||| ||||||||||||||||||||||||||
Db        143 AKLLMDPKRQIFLDQNILGVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202

Qy        181 RIRAVTIDRMMSYLNSS 197
              :|||||||:|||||:|
Db        203 KIRAVTIDRVMSYLNAS 219


RESULT 11
I12A_CAPHI
ID   I12A_CAPHI     STANDARD;      PRT;   221 AA.
AC   O02814;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
```

```
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Beyer J.C., Kumpula-Mcwhirter N.M., Cheevers W.P.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF003542; AAB61287.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    221       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   221 AA;  24832 MW;  58031AAD87199357 CRC64;

  Query Match             82.3%;  Score 818.5;  DB 1;  Length 221;
  Best Local Similarity   83.2%;  Pred. No. 1.3e-65;
  Matches  164;  Conservative   11;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |||| :  ||   ||::|||||||||||||||||||| ||||||||||||||||||||
Db         26 RSLPITTAGPG-RSCLDYSQNLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 84

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||| |||||||||| |||||| |||||| |||| ||| |||:|||||| |||:|:|
Db         85 EACLPLELATNESCLASRETSLITNGHCLASGKTSFMTTLCLRSIYKDLKMYHMEFQAIN 144

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||: |||||| || ||:|||||:| ||||| |||| |||||||:|||||||||
Db        145 AKLLMDPKRQVSLDQNMLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAF 204

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||:||
Db        205 RIRAVTIDRMMSYLSSS 221


RESULT 12
I12A_MARMO
ID   I12A_MARMO     STANDARD;      PRT;   223 AA.
AC   Q61728;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Laxton C.D., Foster G.R., Shanmuganathan S., Mills J.S.,
RA   Ackrill A.M.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X97018; CAA65746.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    223       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     98     98       INTERCHAIN (PROBABLE).
FT   CARBOHYD     41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    121    121       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    176    176       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   223 AA;  24833 MW;  2421024F5A4FFD14 CRC64;

  Query Match             59.6%;  Score 592.5;  DB 1;  Length 223;
  Best Local Similarity   60.0%;  Pred. No. 1.4e-45;
  Matches  120;  Conservative   31;  Mismatches   46;  Indels    3;  Gaps    2;

Qy          1 RSLPTASPSPGIFQ-CLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 59
              |:|| ::| | : | | | || ||  | : || | : || | |::||::|||||::|:|
Db         24 RNLPRSTPVPAVSQECHNLSQTLLSTVDSALQNAIEILEYYPCSAEEVNHEDITKNRTNT 83

Qy         60 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 119
              |:|||| ||  ||:|||||| | |   | | ||: |: | || |||||||||||:| ||:
Db         84 VKACLPQELAQNENCLASRETSFIIKRSSLTSGRTSWNTTLCFSSIYEDLKMYQLELKAI 143

Qy        120 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEP--DFYKTKIKLCILL 177
              : ||||||| ||: |: :| |:| |:||:| |: |||  | | |  : |:|| ||||||
Db        144 SEKLLMDPKGQIYEDKALLAAVDYLMQAVNVNNETVPQTPSPEAPSSNLYRTKTKLCILL 203

Qy        178 HAFRIRAVTIDRMMSYLNSS 197
              || |||||||:|:|||||||
Db        204 HALRIRAVTINRVMSYLNSS 223


RESULT 13
I12A_MOUSE
ID   I12A_MOUSE     STANDARD;      PRT;   215 AA.
AC   P43431;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
```

```
RX   MEDLINE=92268481; PubMed=1350290;
RA   Schoenhaut D.S., Chua A.O., Wolitzky A.G., Quinn P.M., Dwyer C.M.,
RA   Gately M.K., Gubler U.;
RT   "Cloning and expression of murine IL-12.";
RL   J. Immunol. 148:3433-3440(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96257799; PubMed=8647196;
RA   Tone Y., Thompson S.A., Babik J.M., Nolan K.F., Tone M., Raven C.,
RA   Waldmann H.;
RT   "Structure and chromosomal location of the mouse interleukin-12 p35
RT   and p40 subunit genes.";
RL   Eur. J. Immunol. 26:1222-1227(1996).
RN   [3]
RP   SEQUENCE OF 1-5 FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=96144329; PubMed=8557982;
RA   Yoshimoto T., Kojima K., Funakoshi T., Endo Y., Fujita T.,
RA   Nariuchi H.;
RT   "Molecular cloning and characterization of murine IL-12 genes.";
RL   J. Immunol. 156:1082-1088(1996).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M86672; AAA39292.1; -.
DR   EMBL; S82419; AAB37382.1; -.
DR   EMBL; S82412; AAB37382.1; JOINED.
DR   EMBL; S82414; AAB37382.1; JOINED.
DR   EMBL; S82417; AAB37382.1; JOINED.
DR   EMBL; S82418; AAB37382.1; JOINED.
DR   EMBL; D63334; BAA09647.1; -.
DR   MGD; MGI:96539; Il12a.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    215       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    92     92       INTERCHAIN (PROBABLE).
FT   CARBOHYD    89     89       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   215 AA;  24179 MW;  56845B9B66D35A53 CRC64;

  Query Match             55.6%;  Score 553;  DB 1;  Length 215;
  Best Local Similarity   56.6%;  Pred. No. 4.3e-42;
  Matches  111;  Conservative   30;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          2 SLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVE 61
              ||    |  |  :||: |:|||:   : :: ||: |: |||||:|:|||||||:|:|||:: 
Db         20 SLARVIPVSGPARCLSQSRNLLKTTDDMVKTAREKLKHYSCTAEDIDHEDITRDQTSTLK 79

Qy         62 ACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNA 121
               ||||||  ||||||:|| |  | ||||   | | |  ||| |||||||||| ||:|:|| 
Db         80 TCLPLELHKNESCLATRETSSTTRGSCLPPQKTSLMMTLCLGSIYEDLKMYQTEFQAINA 139

Qy        122 KLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFR 181
               |     :|| ||: || |||||:|:|| |  |: ||  : | | |: |:|||||||||
Db        140 ALQNHNHQQIILDKGMLVAIDELMQSLNHNGETLRQKPPVGEADPYRVKMKLCILLHAFS 199

Qy        182 IRAVTIDRMMSYLNSS 197
               | |||:|:| ||:|:
Db        200 TRVVTINRVMGYLSSA 215


RESULT 14
YML7_YEAST
ID   YML7_YEAST     STANDARD;      PRT;  1134 AA.
AC   Q03735;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical 126.1 kDa protein in NDI1-ATR1 intergenic region.
GN   YML117W OR YM8339.02.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RA   Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC   -!- SIMILARITY: TO YEAST YPL184C AND S.POMBE NRD1.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; Z49210; CAA89101.1; -.
DR   SGD; S0004585; YML117W.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   InterPro; IPR003955; RRM_2.
DR   SMART; SM00360; RRM; 1.
DR   SMART; SM00362; RRM_2; 1.
DR   PROSITE; PS50102; RRM; 1.
DR   PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
KW   Hypothetical protein; RNA-binding.
FT   DOMAIN      653    726       RNA-BINDING (RRM).
SQ   SEQUENCE   1134 AA;  126138 MW;  47B0FF7C5B98A053 CRC64;

  Query Match              8.7%;  Score 86.5;  DB 1;  Length 1134;
  Best Local Similarity   24.8%;  Pred. No. 7.5;
  Matches   50;  Conservative   27;  Mismatches   54;  Indels   71;  Gaps   12;

Qy         15 CLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDH----EDITKD--KTSTVEACLPLE- 67
                |:|:       |  |   | :|  |     | :||      | |:  |::|:|:   :| 
Db        198 CINYK------VLPTGDDAYRTRSL---LIENVDHSIDLHSIVKNFVKSNTLESAYLIEG 248

Qy         68 ---------LTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFK- 117
                      | | | |    || :| | ||             : | ::     |||  
Db        249 GKSDDSKDVETKNLSIL----ISFLTKGDCL-------------NFYNNILQRLSEFKT 290

Qy        118 -----AMNAK---LLMDPK-RQIFLDQNMLTAIDE----------LLQALNFN------- 151
                  |:| |   |  |||    |::   ||   |          :  :|: |        
Db        291 FLKSEALNLKFVCLNYDPKCLPTFIESEALTENAEEADITNGSTMISASLHHNIANKDAT 350

Qy        152 -SVTVPQKSSLEEPDFYKTKIK 172
                |: :  || :|: | :| |::
Db        351 RSIIIEFKSPVEKSDLFKKKLQ 372


RESULT 15
YD86_SCHPO
ID   YD86_SCHPO     STANDARD;      PRT;  1957 AA.
AC   Q10411;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Hypothetical protein C1F3.06c in chromosome I.
```

```
GN   SPAC1F3.06C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; Z70690; CAA94624.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   1957 AA;  222785 MW;  3F480CA06171D9DA CRC64;

  Query Match             8.6%;  Score 85.5;  DB 1;  Length 1957;
  Best Local Similarity   20.4%;  Pred. No. 18;
  Matches   46;  Conservative   47;  Mismatches   78;  Indels   55;  Gaps    8;

Qy          3 LPTASPSPGIFQCL-NHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHE---------- 50
              | :|    |  | | : | :|:  : : ||:|:: :::   | :|:|||
Db       1476 LASAVEKLGALQKLHSESLSLMENIKSQLQEAKEKIQVDESTIQELDHEITASKNNYEGK 1535

Qy         51 -----DITKDKTSTVEA---CLPLELTMNESCLASREISLITNGSCLAS---------- 91
                  | :| :  :|     |  | :  :     :|  ::   | ||
Db       1536 LNDKDSIIRDLSENIEQLNNLLAEEKSAVKRLSTEKESEILQFNSRLADLEYHKSQVESE 1595

Qy         92 -GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNF 150
               |::     | |:|  |:|:: : |  ::  ::| | : |:    |:  :: | |: |
Db       1596 LGRSK----LKLASTTEELQLAENERLSLTTRML-DLQNQVKDLSNIKDSLSEDLRTLR- 1649

Qy        151 NSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNS 196
                  |||:          :  |    :|:: |:: :   | |
Db       1650 ---------SLED--------SVASLQKECKIKSNTVESLQDVLTS 1678


Search completed: July 15, 2003, 11:07:00
Job time : 5.31729 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:57:19 ; Search time 17.4569 Seconds
(without alignments)
2325.231 Million cell updates/sec

Title: US-09-917-265-50
Perfect score: 994
Sequence: 1 RSLPTASPSPGIFQCLNHSQ.....HAFRIRAVTIDRMMSYLNSS 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	875	88.0	253	4	O60595	O60595 homo sapien
2	768	77.3	221	11	Q924V6	Q924v6 cavia porce
3	644	64.8	215	11	Q91ZK6	Q91zk6 sigmodon hi
4	588.5	59.2	223	11	Q9ET04	Q9et04 marmota mon
5	562	56.5	215	11	Q9R103	Q9r103 rattus norv
6	523	52.6	210	11	Q924K6	Q924k6 meriones un
7	441	44.4	94	6	O62777	O62777 felis silve
8	272	27.4	61	6	Q9MYW1	Q9myw1 bos taurus
9	232	23.3	116	11	Q9QUT1	Q9qut1 mus musculu
10	97.5	9.8	816	10	Q9SJT3	Q9sjt3 arabidopsis
11	95	9.6	444	4	Q9NXJ6	Q9nxj6 homo sapien
12	93	9.4	1583	16	Q92GE9	Q92ge9 rickettsia
13	90	9.1	537	5	Q9VZU0	Q9vzu0 drosophila
14	90	9.1	581	10	O04143	O04143 silene lati
15	90	9.1	615	5	Q18809	Q18809 caenorhabdi
16	89	9.0	539	4	Q9HCC8	Q9hcc8 homo sapien
17	89	9.0	547	2	Q8RJP4	Q8rjp4 alteromonas
18	88.5	8.9	383	16	O84156	O84156 chlamydia t
19	87.5	8.8	273	4	Q9Y448	Q9y448 homo sapien
20	87	8.8	488	10	Q948S0	Q948s0 athyrium yo
21	86.5	8.7	924	5	O15738	O15738 dictyosteli
22	86	8.7	1286	5	Q21025	Q21025 caenorhabdi
23	84.5	8.5	243	12	Q66085	Q66085 canine herp
24	84.5	8.5	310	5	Q9TZ87	Q9tz87 caenorhabdi
25	84	8.5	849	16	Q97E36	Q97e36 clostridium
26	84	8.5	1200	10	Q9FQL7	Q9fql7 zea mays (m
27	83	8.4	826	13	Q9PVN6	Q9pvn6 xenopus lae
28	83	8.4	1061	13	Q9PVN7	Q9pvn7 xenopus lae
29	83	8.4	1869	12	Q998P7	Q998p7 broad bean
30	82.5	8.3	271	16	Q8Y6E9	Q8y6e9 listeria mo
31	82.5	8.3	523	2	Q9S6P3	Q9s6p3 chlamydia p
32	82.5	8.3	523	16	Q9Z9G2	Q9z9g2 chlamydia p
33	82.5	8.3	607	16	O25379	O25379 helicobacte
34	82.5	8.3	640	16	Q9WZB2	Q9wzb2 thermotoga
35	82	8.2	595	11	Q922L3	Q92213 mus musculu
36	82	8.2	649	5	O44633	O44633 caenorhabdi
37	82	8.2	1312	11	Q9JIL8	Q9jil8 rattus norv
38	81.5	8.2	446	10	Q9M0E1	Q9m0e1 arabidopsis
39	81.5	8.2	460	4	Q9H8M0	Q9h8m0 homo sapien
40	81.5	8.2	541	4	Q8TBY2	Q8tby2 homo sapien
41	81.5	8.2	649	4	Q9H0T2	Q9h0t2 homo sapien
42	81.5	8.2	2263	5	Q9W0L0	Q9w0l0 drosophila
43	81.5	8.2	8805	5	Q9V6V4	Q9v6v4 drosophila
44	81	8.1	314	16	Q98Q43	Q98q43 mycoplasma
45	81	8.1	318	2	Q9L8P4	Q9l8p4 mycoplasma

ALIGNMENTS

RESULT 1
O60595
ID O60595 PRELIMINARY; PRT; 253 AA.
AC O60595;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin 12 (Interleukin-12 P35 subunit).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Guo Y., Wu M.;
RT "Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
RT Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-39 FROM N.A.
RC TISSUE=PLACENTA;
RA Hayes M.P., Murphy F.J., Burd P.R.;
RL Blood 0:0-0(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Hongyuan J., Meiyun Z.;
RT "Cloning and sequence analysis of IL-12 cDNA from Chinese.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF101062; AAD16432.1; -.
DR EMBL; AF050083; AAC05211.1; -.
DR EMBL; AF180562; AAD56385.1; -.
DR InterPro; IPR002106; AAtRNA_ligaseII.
DR InterPro; IPR004281; IL12.
DR Pfam; PF03039; IL12; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
FT VARIANT 247 247 M -> T.
SQ SEQUENCE 253 AA; 28293 MW; FAC56ACD2A620BD5 CRC64;

Query Match 88.0%; Score 875; DB 4; Length 253;

```
  Best Local Similarity   86.8%;  Pred. No. 1.5e-73;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db         57 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 116

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||| ||||| ||| | ||||||||| | ||| ||||||||||||||:||| ||
Db        117 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 176

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||  ||||:|||||| ||||||||||||||||||||||||||||
Db        177 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 236

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        237 RIRAVTIDRVMSYLNAS 253


RESULT 2
Q924V6
ID   Q924V6      PRELIMINARY;      PRT;   221 AA.
AC   Q924V6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p35 subunit (IL-12 p35).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HARTLEY;
RA   Shiratori I., Matsumoto M., Tsuji S., Nomura M., Toyoshima K.,
RA   Seya T.;
RT   "Molecular cloning and functional characterization of guinea pig
RT   Interleukin -12.";
RL   Int. Immunol. 0:0-0(2001).
DR   EMBL; AB025723; BAB63962.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SQ   SEQUENCE   221 AA;  24687 MW;  972E59F5A11DE896 CRC64;

  Query Match           77.3%;  Score 768;  DB 11;  Length 221;
  Best Local Similarity   76.9%;  Pred. No. 1.1e-63;
  Matches  153;  Conservative   17;  Mismatches   27;  Indels    2;  Gaps    1;

Qy          1 RSLPTASPSPGI--FQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTS 58
              |:|| |||:|     || |||| |||||:: | || | | :|||| ||||||||||||||
Db         23 RNLPRASPAPVTEPVQCFNHSQTLLRAVNSELHKAIQMLAVYSCTPEEIDHEDITKDKTS 82

Qy         59 TVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKA 118
              ||:||:|||| |||||||  || ||||||||||| |||  |||:|||||||:||:|||
Db         83 TVKACVPLELVKNESCLASGHISFTTNGSCLASGKTSFMMALCLNSIYEDLKLYQLEFKN 142

Qy        119 MNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLH 178
              |||:|||||:|||||||||:|||||:|||| : |||||| ||||||||| |:|||||||
Db        143 MNAQLLMDPQRQIFLDQNMLSAIDELIQALNGSDVTVPQKLSLEEPDFYKIKMKLCILLH 202

Qy        179 AFRIRAVTIDRMMSYLNSS 197
              |||||||||||:|||| ||
Db        203 AFRIRAVTIDRVMSYLTSS 221


RESULT 3
Q91ZK6
ID   Q91ZK6      PRELIMINARY;      PRT;   215 AA.
AC   Q91ZK6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin 12 p35 subunit.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Blanco J.C., Pletneva L.M., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF421396; AAL16937.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   215 AA;  24042 MW;  435DF86A7D72A244 CRC64;

  Query Match           64.8%;  Score 644;  DB 11;  Length 215;
  Best Local Similarity   66.0%;  Pred. No. 3.8e-52;
  Matches  130;  Conservative   24;  Mismatches   39;  Indels    4;  Gaps    1;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |: | ::|:    ||| |||||||  :: |:|| |||: | ||:|:|||||||:|||||:
Db         23 RATPVSTPA----QCLAHSQNLLRTTNHMLEKAIQTLKHYPCTAEDIDHEDITEDKTSTL 78

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||| ||  |||| || : | :| ||||   | | |  ||||||||||||||| ||||:|
Db         79 NACLPPELAKNESCWASGKTSSVTRGSCLPPQKTSSMMTLCLSSIYEDLKMYQTEFKAIN 138

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |:||   ::|| ||:||||||||||:|||| |  | ||| |||| | || ||||||||||
Db        139 AELLDHNRKQIILDENMLTAIDELMQALNLNGETRPQKPSLEEADPYKVKIKLCILLHAF 198

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||:||:|:|||||||:
Db        199 SIRAITINRVMSYLNSA 215


RESULT 4
Q9ET04
ID   Q9ET04      PRELIMINARY;      PRT;   223 AA.
AC   Q9ET04;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-12 p35 subunit.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21424491; PubMed=11533170;
RA   Garcia-Navarro R., Blanco-Urgoiti B., Berraondo P.,
RA   Sanchez De La Rosa R., Vales A., Hervas-Stubbs S., Lasarte J.J.,
RA   Borras F., Ruiz J., Prieto J.;
RT   "Protection against Woodchuck Hepatitis Virus (WHV) Infection by Gene
RT   Gun Coimmunization with WHV Core and Interleukin-12.";
RL   J. Virol. 75:9068-9076(2001).
DR   EMBL; AF288520; AAG01024.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   223 AA;  24831 MW;  2423E5498A4FFD14 CRC64;

  Query Match           59.2%;  Score 588.5;  DB 11;  Length 223;
  Best Local Similarity   59.5%;  Pred. No. 5.8e-47;
  Matches  119;  Conservative   31;  Mismatches   47;  Indels    3;  Gaps    2;

Qy          1 RSLPTASPSPGIFQ-CLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 59
              |:|| ::| | : | | | || ||  | : || | : || | |::||::|||||::|:|:|
Db         24 RNLPRSTPVPAVSQECHNLSQTLLSTVDSALQNAIEILEYYPCSAEEVNHEDITKNRTNT 83
```

```
Qy          60 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 119
               |:|||| ||  ||:|||||| | |   | | ||: |: | || ||||||||||:| ||:
Db          84 VKACLPQELAQNENCLASRETSFIIKRSSLTSGRTSWNTTLCFSSIYEDLKMYQLELKAI 143

Qy         120 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLE--EPDFYKTKIKLCILL 177
               : ||||||| ||: |: :| |:| |:||:| |: |||| | |   |: |:|| |||||
Db         144 SEKLLMDPKGQIYEDKALLAAVDYLMQAVNVNNETVPQTPSPEAPSPNLYRTKTKLCILL 203

Qy         178 HAFRIRAVTIDRMMSYLNSS 197
               || |||||| :|:|||||||
Db         204 HALRIRAVTTNRVMSYLNSS 223


RESULT 5
Q9R103
ID   Q9R103      PRELIMINARY;      PRT;   215 AA.
AC   Q9R103;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 p35 subunit.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DA;
RA   Verma N.D., He X.Y., Hall B.M.;
RT   "Cloning of the rat interleukin 12 p35 subunit.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177031; AAD51364.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   215 AA;  24246 MW;  60EDC00C70F0E005 CRC64;

  Query Match             56.5%;  Score 562;  DB 11;  Length 215;
  Best Local Similarity   56.9%;  Pred. No. 1.6e-44;
  Matches  112;  Conservative   34;  Mismatches   47;  Indels    4;  Gaps    1;

Qy           1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
               | :| : |:    :||| ||||:   : :: ||: |: |||| : :|||||||:||||||:
Db          23 RVIPVSGPA----KCLNQSQNLLKTTDDMVRTAREKLKHYSCTAGDIDHEDITRDKTSTL 78

Qy          61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
               |||||||| ||||||::| | |  |||   | | |  ||| |||||||||| ||:|:|
Db          79 EACLPLELHKNESCLATKETSSIIRGSCLPPQKTSLMMTLCLGSIYEDLKMYQSEFQAIN 138

Qy         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
               | |     :|| ||:||| ||||||:::|| :  |: ||: : | | |: |:||||||||||
Db         139 AALQSHNHQQITLDRNMLMAIDELMRSLNHSGETLHQKAPMGEADPYRVKMKLCILLHAF 198

Qy         181 RIRAVTIDRMMSYLNSS 197
                 | :||:|:|:||:||
Db         199 STRVMTINRVMNYLSSS 215


RESULT 6
Q924K6
ID   Q924K6      PRELIMINARY;      PRT;   210 AA.
AC   Q924K6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-12 p35 subunit.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gaucher D., Chadee K.;
RT   "Molecular cloning of gerbil interleukin-12, and its expression as a
RT   bioactive single-chain protein.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288849; AAK83072.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   210 AA;  23742 MW;  5D44D9E2BFA0BB70 CRC64;

  Query Match             52.6%;  Score 523;  DB 11;  Length 210;
  Best Local Similarity   58.7%;  Pred. No. 6.8e-41;
  Matches  115;  Conservative   22;  Mismatches   55;  Indels    4;  Gaps    3;

Qy           2 SLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVE 61
               ||  | |  |  :||| || |||   | |: ||| |  | | :|: | ||||||||||::
Db          19 SLARAKPVSGPARCLNSSQTLLRTTDNALKTARQKLTNY-CGAEDFDREDITKDKTSTLK 77

Qy          62 ACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNA 121
               |||||||  ||||||    |:|  ||||   | | |  ||||||||||:|| ||:|::|
Db          78 ACLPLELVKNESCLAGETSSMI-RGSCLLPQKTSSMMTLCLSSIYEDLKIYQTEFQAIDA 136

Qy         122 KLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFR 181
               :|    : || ||::|| |||||:|||| |  |||:|  | | |  | :: ||| ||||
Db         137 ELRR--QNQITLDKDMLAAIDELMQALNHNGQTVPRKPYLAERDPIKLEMHLCIQLHAFS 194

Qy         182 IRAVTIDRMMSYLNSS 197
               ||  ||:::|||||||
Db         195 IRVTTINKVMSYLNSS 210


RESULT 7
O62777
ID   O62777      PRELIMINARY;      PRT;    94 AA.
AC   O62777;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 p35 subunit (Fragment).
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99322318; PubMed=10391845;
RA   Harley R., Helps C.R., Harbour D.A., Gruffydd-Jones T.J., Day M.J.;
RT   "Cytokine mRNA expression in lesions in cats with chronic
RT   gingivostomatitis.";
RL   Clin. Diagn. Lab. Immunol. 6:471-478(1999).
DR   EMBL; AF054605; AAC15978.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
FT   NON_TER       1       1
FT   NON_TER      94      94
SQ   SEQUENCE   94 AA;  10616 MW;  AD67866E916201AD CRC64;

  Query Match             44.4%;  Score 441;  DB 6;  Length 94;
  Best Local Similarity   92.6%;  Pred. No. 1.1e-33;
  Matches   87;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          22 LLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREIS 81
               ||||:|||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db           1 LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREIS 60

Qy          82 LITNGSCLASGKASFMTVLCLSSIYEDLKMYQME 115
               |||||||||| | |||| |||||||||||||:|
Db          61 LITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE 94


RESULT 8
Q9MYW1
ID   Q9MYW1      PRELIMINARY;      PRT;    61 AA.
AC   Q9MYW1;
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DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12 polypeptide 35 (Fragment).
GN   IL-12 P35.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20539119; PubMed=11086544;
RA   Schmidt P., Kuehn C., Kang'a S., Hanotte O., Vanselow J., Anton I.,
RA   Langner C., Schwerin M.;
RT   "Interleukin-12 p35 encoding gene of cattle and sheep harbours a
RT   polymorphic T stretch in intron 4.";
RL   Anim. Genet. 31:283-283(2000).
DR   EMBL; AJ271034; CAB97049.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
FT   NON_TER       1      1
FT   NON_TER      61     61
SQ   SEQUENCE   61 AA;  6699 MW;  9C32147DB2BFA1A4 CRC64;

  Query Match             27.4%;  Score 272;  DB 6;  Length 61;
  Best Local Similarity   86.9%;  Pred. No. 3.7e-18;
  Matches   53;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         48 DHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYE 107
              ||||||||||||||||||||  |||||||| | |||| |||||| |||| ||| ||||
Db          1 DHEDITKDKTSTVEACLPLELATNESCLASRETSFITNGHCLASGKTSFMTTLCLRSIYE 60

Qy        108 D 108
              |
Db         61 D 61


RESULT 9
Q9QUT1
ID   Q9QUT1      PRELIMINARY;      PRT;   116 AA.
AC   Q9QUT1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12A.
GN   IL12A OR LL12A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SJL/J, AND B10.S/J; TISSUE=SPLEEN;
RA   Ma R.Z., Teuscher C.;
RT   "Screening for candidate genes of mouse autoimmnue diseases.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF128211; AAF22552.1; -.
DR   EMBL; AF128210; AAF22551.1; -.
DR   MGD; MGI:96539; Il12a.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
SQ   SEQUENCE   116 AA;  12954 MW;  06777BF8D56AAAFE CRC64;

  Query Match             23.3%;  Score 232;  DB 11;  Length 116;
  Best Local Similarity   54.2%;  Pred. No. 4.1e-14;
  Matches   45;  Conservative   16;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 SLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVE 61
              ||     |  |  :||: |:|||:   : :: ||: |: ||||:|:|||||||:|:|||::
Db         20 SLARVIPVSGPARCLSQSRNLLKTTDDMVKTAREKLKHYSCTAEDIDHEDITRDQTSTLK 79

Qy         62 ACLPLELTMNESCLASREISLIT 84
                ||||||  |||||||:|| |  |
Db         80 TCLPLELHKNESCLATRETSSTT 102


RESULT 10
Q9SJT3
ID   Q9SJT3      PRELIMINARY;      PRT;   816 AA.
AC   Q9SJT3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   At2g21450 protein.
GN   AT2G21450.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA   Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA   Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA   Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA   Salzberg S.L., Fraser C.M., Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Lin X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC006841; AAD23689.1; -.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR000330; SNF2_N.
DR   Pfam; PF00271; helicase_C; 1.
DR   Pfam; PF00176; SNF2_N; 2.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
KW   ATP-binding; Helicase.
SQ   SEQUENCE   816 AA;  93297 MW;  A5B249A1C2FF7A9C CRC64;

  Query Match             9.8%;  Score 97.5;  DB 10;  Length 816;
  Best Local Similarity   23.2%;  Pred. No. 1.3;
  Matches   52;  Conservative   34;  Mismatches   79;  Indels   59;  Gaps    9;

Qy         20 QNLLRAVSNTLQKARQ-------TLELYS--CTSEEIDHEDITKDKTSTVEACL--PLEL 68
              || :  | | |   |         | |: |   :  ||        :|::|      :||
Db        442 QNNVEEVFNILDLVRPKFLKRPGTREIVSRIMSKAEIPRGKQVNQSSSSIEGTFFAAVEL 501

Qy         69 TMNESCLASREISLI--------------TNGSCLASGKASFMTVLCLSSIYED----- 108
              |:  |   | : |||                : | |  | : |  :| ||||  |
Db        502 TLQRSTNFSAKASLIKDLREMTRNILHYHKADFSGLLPGLSEFTVMLNLSSIQRDEVKGL 561

Qy        109 LKMYQMEFKAMNAKLLMDPKRQIFLDQN------------MLTAIDELLQALNFNSVTV 155
               ||   :  :: | | : || : ||::|              :  :|::|: :|     |
Db        562 RKMELFKQISLGAALYIHPKLKSFLEENPSNGEKGFSDNNTTVMKLDKMLKKINVRD-GV 620

Qy        156 PQKSSLEEPDFYKTKIKLC-------ILLHAFRIRAVTIDRMMS 192
              |       |:   : ||       ::   : :   |::|:||
Db        621 KMK-------FFLNLLALCESTGEKLLVFSQYIVPIKTLERLMS 657


RESULT 11
Q9NXJ6
ID   Q9NXJ6      PRELIMINARY;      PRT;   444 AA.
AC   Q9NXJ6;
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DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CDNA FLJ20207 fis, clone COLF1609.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON MUCOSA;
RA   Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA   Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
RA   Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK000214; BAA91014.1; -.
DR   InterPro; IPR000583; GATase_2.
DR   InterPro; IPR004129; GDPD.
DR   Pfam; PF03009; GDPD; 1.
DR   PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
SQ   SEQUENCE   444 AA;  50585 MW;  52AF60FF1F76B6E5 CRC64;

  Query Match             9.6%;  Score 95;  DB 4;  Length 444;
  Best Local Similarity   21.4%;  Pred. No. 1.1;
  Matches   51;  Conservative   30;  Mismatches   87;  Indels   70;  Gaps   10;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEID----------H 49
              | ||   | ||:   : |    : |  |||   |:| |    |  | |
Db        218 RDLP---PKPGL---VGHRGAPMLAPENTLMSLRKTAEC-GATVFETDVMVSSDGVPFLM 270

Qy         50 EDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGK--------------A 94
                |    :|: | :  |  :| : |  :  |:  :  ||    :              |
Db        271 HDEHLSRTTNVASVFPTRITAHSSDFSWTELKRLNAGSWFLERRPFWGAKPLAGPDQKEA 330

Qy         95 SFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMD----PKRQIFLDQNMLTAIDELL----- 145
                ||  |  : |       |  |:|  :: |    |:   : |  ::  :: :|
Db        331 ESQTVPALEELLE-------EAAALNLSIMFDLRRPPQNHTYYDTFVIQTLETVLNARVP 383

Qy        146 QALNF-----------------NSVTVPQKSSLEEPDFYKTKIKLC---ILLHAFRI 182
              ||: |                 : | : :    | |  : ||:|   |  |  ||
Db        384 QAMVFWLPDEDRAMSNDGHLECARYMDVREATERGGPSFLTSPIKICHYWISRHCIRI 441


RESULT 12
Q92GE9
ID   Q92GE9      PRELIMINARY;      PRT;  1583 AA.
AC   Q92GE9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical protein RC1174.
GN   RC1174.
OS   Rickettsia conorii.
OC   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia.
OX   NCBI_TaxID=781;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MALISH 7;
RX   MEDLINE=21442074; PubMed=11557893;
RA   Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA   Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA   Raoult D.;
RT   "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL   Science 293:2093-2098(2001).
DR   EMBL; AE008665; AAL03712.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   1583 AA;  181365 MW;  FB3FE733C2872625 CRC64;

  Query Match             9.4%;  Score 93;  DB 16;  Length 1583;
  Best Local Similarity   22.6%;  Pred. No. 7.4;
  Matches   47;  Conservative   40;  Mismatches   71;  Indels   50;  Gaps    9;

Qy          9 SPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLEL 68
              | |:  | :|  |:  |:|: :   : |||          :   :  | |  ||     ||
Db       1140 SAGV-DCSDHEVNIKIALSSAITSGKITLE---------ERNKLLNDMTKQVE-----EL 1184

Qy         69 TMNESCLASREISLITNGSCLASGKASFMTVLCLS---SIYEDLKMYQME---------- 115
                : ::   :  |:::     |        ||  ||    | |: |: : |
Db       1185 VLIDNYKQTEAITIMQLSPTL--------TVNILSQFIDILEEEKVLERENEFLPSAEEL 1236

Qy        116 -FKAMNAKLLMDPKRQIFLDQNMLTAIDELLQAL-----NFNSVTVPQKSSLEEPDFYKT 169
               :||: ::|  |:  | |  :  :|  ||: :       |::  :        |:  :
Db       1237 NSRAMSGEVLTRPELCILLSYSKRSAYHELINSTFSHDKYFDAYLIDY-----FPEMMQK 1291

Qy        170 KIKLCILLHAFR---IRAVTIDRMMSYL 194
              | :  || |  :   |: |||:::|: |
Db       1292 KFRNEILSHPLKHEIIKTVTINKIMNQL 1319


RESULT 13
Q9VZU0
ID   Q9VZU0      PRELIMINARY;      PRT;  537 AA.
AC   Q9VZU0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CG12032 protein.
GN   CG12032.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
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RL   Science 287:2185-2195(2000).
DR   EMBL; AE003477; AAF47727.1; -.
DR   FlyBase; FBgn0035408; CG12032.
DR   InterPro; IPR000051; SAM_bind.
DR   InterPro; IPR003402; Unk_Met10.
DR   Pfam; PF02475; Met_10; 1.
SQ   SEQUENCE   537 AA;  61413 MW;  686BC8CBBBCC70D4 CRC64;

  Query Match             9.1%;  Score 90;  DB 5;  Length 537;
  Best Local Similarity   25.1%;  Pred. No. 4;
  Matches   47;  Conservative   29;  Mismatches   75;  Indels   36;  Gaps   11;

Qy          2 SLPTASP---------SPGIFQCLNHSQNLLRAVSN---TLQKARQTLELYSCTSEEIDH 49
              |:| |           :|  |: | |:    : : |   : :  || :       ||:
Db        241 SIPAAKKRCHVLANDLNPESFRWLQHNAKRNKCLPNIKMSNKDGRQFI------VEEL-R 293

Qy         50 EDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDL 109
              ||: |   :|      : :|||   :|   :     |   |   |   | :|    |  :
Db        294 EDLLKRLCTTDTTTYGIHITMNLPAMAVEFLDAF-RGLYSADELAQLPTNVC----YPTV 348

Qy        110 KMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDE-LLQALNFNSVTVPQKSSLEEPDFYK 168
               :|    |  | | |:   ||: :: |:  ::|| ||| :||     | |       | |:
Db        349 HVYSFA-KGENTKELV---RQL-VESNLGASLDENLLQGINFVRNVAPNK------DMYR 397

Qy        169 TKIKLCI 175
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Db        398 VSFKLSL 404


RESULT 14
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ID   O04143      PRELIMINARY;      PRT;   581 AA.
AC   O04143;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 63.5 kDa protein.
OS   Silene latifolia (White campion).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX   NCBI_TaxID=37657;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FLOWERBUDS;
RX   MEDLINE=98042964; PubMed=9375394;
RA   Barbacar N., Hinnisdaels S., Farbos I., Moneger F., Lardon A.,
RA   Delichere C., Mouras A., Negrutiu I.;
RT   "Isolation of early genes expressed in reproductive organs of the
RT   dioecious white campion (Silene latifolia) by subtraction cloning
RT   using an asexual mutant.";
RL   Plant J. 12:805-817(1997).
DR   EMBL; Y12529; CAA73132.1; -.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR003592; LRR_out.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00560; LRR; 17.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00370; LRR; 5.
DR   SMART; SM00369; LRR_TYP; 4.
KW   Hypothetical protein.
SQ   SEQUENCE   581 AA;  63516 MW;  52E2D16AD1AA3642 CRC64;

  Query Match             9.1%;  Score 90;  DB 10;  Length 581;
  Best Local Similarity   21.7%;  Pred. No. 4.4;
  Matches   59;  Conservative   42;  Mismatches   75;  Indels   96;  Gaps   13;

Qy          4 PTAS---------PSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYS----------CTS 44
              |||:          ||    | :  |:: : |::: |    : | |            | |
Db        321 PTAALLKYLRGRLPSAEEAQVMTPSKDNMVAMASRLSITTKELSLVGMGLIAVPPEVCES 380

Qy         45 EEIDHEDITKDKTS----TVEACLPLELTM----------------NESCL------- 75
                ||   |::|:       |: ||  ||: :                | :||

Db        381 NEITKVDLSKNSIQELPVTLSACSSLEVLILSRNKIKDWPEDALKSLPNLTCLRLDNNPL 440

Qy         76 ---------ASREISLITNGSCLAS--GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLL 124
                       |   : ::    |::|     :| ::  |  :|    : ::: : : : :|
Db        441 NKVPLNGFDAVPRLQILDLSGCVSSLVDNPAFASLQHLVELY----LRRVKLQEVPSDIL 496

Qy        125 MDPKRQIF-LDQNMLTAIDELLQ--------ALNFNSV-TVPQKSSLEEPDFYKTKIKLC 174
              |  | ||  | || | :| :  |          |: ||: |:| :  | ||
Db        497 MLRKLQILDLSQNSLHSIPQGFQNLTSLTELDLSDNSIGTLPPELGLLEPS--------- 547

Qy        175 ILLHAFR--------IRAVTIDR----MMSYL 194
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Db        548 --LQALRLDGNPLRSIRRTILDRGTKAVLQYL 577


RESULT 15
Q18809
ID   Q18809      PRELIMINARY;      PRT;   615 AA.
AC   Q18809;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   C53D6.6 protein.
GN   C53D6.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gardner A.E.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z70270; CAA94225.1; -.
SQ   SEQUENCE   615 AA;  70011 MW;  FF4C6F4C18EB5A75 CRC64;

  Query Match             9.1%;  Score 90;  DB 5;  Length 615;
  Best Local Similarity   25.1%;  Pred. No. 4.7;
  Matches   43;  Conservative   30;  Mismatches   62;  Indels   36;  Gaps    9;

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              ||| |: : | ||  :| ||   :    |:        |  :| |  :   :||| :
Db        251 VSN-LKLSAQLLEFDIYDCTWNSLSLASISGINTIPGGTELIEKCKKIVQKINESAVYET 309

Qy         79 ----EISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLD 134
                  |   | :   : ||| :::||:   |::|       : | :    ||:    : |
Db        310 SLIGEYMTIDSADLVKSGKLNWITVV---SMFEQF----TKLKGLLDTFLMNDMEGLMLY 362

Qy        135 QNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAV 185
              |    :: :|: |:      | |:::   || |         | ||| |:
Db        363 QQDYDLMEIILRTLS------PLKTAV---DFGKQ--------HTFRISAI 396


Search completed: July 15, 2003, 11:06:07
Job time : 18.4569 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:59:19 ; Search time 6.7575 Seconds
(without alignments)
857.760 Million cell updates/sec

Title: US-09-917-265-50
Perfect score: 994
Sequence: 1 RSLPTASPSPGIFQCLNHSQ.....HAFRIRAVTIDRMMSYLNSS 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	875	88.0	219	1	US-08-186-529-4	Sequence 4, Appli
2	875	88.0	219	1	US-08-640-386A-4	Sequence 4, Appli
3	875	88.0	253	1	US-08-265-087-4	Sequence 4, Appli
4	875	88.0	253	1	US-08-621-493-4	Sequence 4, Appli
5	875	88.0	253	2	US-08-684-687-4	Sequence 4, Appli
6	875	88.0	253	2	US-08-965-688-4	Sequence 4, Appli
7	875	88.0	253	4	US-09-260-173-4	Sequence 4, Appli
8	869	87.4	219	2	US-08-751-767A-2	Sequence 2, Appli
9	868	87.3	519	2	US-08-751-767A-12	Sequence 12, Appl
10	868	87.3	540	2	US-08-751-767A-8	Sequence 8, Appli
11	868	87.3	540	2	US-08-751-767A-10	Sequence 10, Appl
12	553	55.6	215	2	US-08-385-335A-12	Sequence 12, Appl
13	553	55.6	215	2	US-08-659-206A-2	Sequence 2, Appli
14	553	55.6	215	2	US-08-659-206A-5	Sequence 5, Appli
15	84.5	8.5	2482	1	US-08-328-254-6	Sequence 6, Appli
16	83.5	8.4	3248	1	US-08-353-700-1	Sequence 1, Appli
17	83.5	8.4	3248	5	PCT-US95-16216-1	Sequence 1, Appli
18	78	7.8	1786	2	US-08-477-451-16	Sequence 16, Appl
19	77.5	7.8	143	2	US-08-477-451-37	Sequence 37, Appl
20	77	7.7	1091	3	US-08-986-485-5	Sequence 5, Appli
21	73	7.3	226	4	US-09-134-001C-3578	Sequence 3578, Ap
22	73	7.3	273	1	US-08-137-175A-5	Sequence 5, Appli
23	73	7.3	273	4	US-08-479-017-5	Sequence 5, Appli
24	73	7.3	273	4	US-09-196-293-13	Sequence 13, Appl
25	73	7.3	273	4	US-08-209-603E-13	Sequence 13, Appl
26	73	7.3	338	2	US-08-441-857-10	Sequence 10, Appl
27	73	7.3	338	3	US-08-193-159-10	Sequence 10, Appl
28	73	7.3	816	1	US-08-190-802A-54	Sequence 54, Appl
29	73	7.3	816	4	US-08-477-346-54	Sequence 54, Appl
30	73	7.3	816	4	US-08-473-089-54	Sequence 54, Appl
31	73	7.3	816	4	US-08-487-072A-54	Sequence 54, Appl
32	72.5	7.3	451	2	US-08-372-652-2	Sequence 2, Appli
33	72.5	7.3	451	5	PCT-US95-16311-2	Sequence 2, Appli
34	72.5	7.3	472	1	US-08-496-631-2	Sequence 2, Appli
35	72.5	7.3	484	2	US-08-372-652-1	Sequence 1, Appli
36	72.5	7.3	484	5	PCT-US95-16311-1	Sequence 1, Appli
37	72.5	7.3	2938	5	PCT-US94-00198-3	Sequence 3, Appli
38	72	7.2	340	3	US-08-705-771-20	Sequence 20, Appl
39	72	7.2	928	4	US-08-328-673A-8	Sequence 8, Appli
40	72	7.2	1048	4	US-08-887-534A-85	Sequence 85, Appl
41	71.5	7.2	146	2	US-08-788-943A-12	Sequence 12, Appl
42	71.5	7.2	146	2	US-08-788-943A-13	Sequence 13, Appl
43	71.5	7.2	146	5	PCT-US96-00952-10	Sequence 10, Appl
44	71.5	7.2	146	5	PCT-US96-00952-11	Sequence 11, Appl
45	71.5	7.2	3457	2	US-08-416-603-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-08-186-529-4
; Sequence 4, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-186-529-4

  Query Match             88.0%;  Score 875;  DB 1;  Length 219;
  Best Local Similarity   86.8%;  Pred. No. 1.7e-92;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| ||||||||| | |||||||||||||||||||
Db         23 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
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Db         83 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 142

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              ||||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||
Db        143 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202

Qy        181 RIRAVTIDRMMSYLNSS 197
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Db        203 RIRAVTIDRVMSYLNAS 219


RESULT 2
US-08-640-386A-4
; Sequence 4, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-640-386A-4

  Query Match             88.0%;  Score 875;  DB 1;  Length 219;
  Best Local Similarity   86.8%;  Pred. No. 1.7e-92;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:||||||||||| |||||||| | ||||||||||||||||||
Db         23 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||| ||||| ||| | ||||||||| | |||  |||||||||||||:||| ||
Db         83 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 142

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||
Db        143 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        203 RIRAVTIDRVMSYLNAS 219


RESULT 3
US-08-265-087-4
; Sequence 4, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  253 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-265-087-4

  Query Match             88.0%;  Score 875;  DB 1;  Length 253;
  Best Local Similarity   86.8%;  Pred. No. 2.2e-92;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:||||||||||| |||||||| | ||||||||||||||||||
Db         57 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 116

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||| ||||| ||| | ||||||||| | |||  |||||||||||||:||| ||
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Qy        181 RIRAVTIDRMMSYLNSS 197
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Db        237 RIRAVTIDRVMSYLNAS 253


RESULT 4
US-08-621-493-4
; Sequence 4, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
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;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  253 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-621-493-4

  Query Match             88.0%;  Score 875;  DB 1;  Length 253;
  Best Local Similarity   86.8%;  Pred. No. 2.2e-92;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db         57 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 116

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||| ||||| ||| | |||||||| | |||  ||||||||||||||:||| ||
Db        117 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 176

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||  ||||:|||||| ||||||||||||||||||||||||||||
Db        177 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 236

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        237 RIRAVTIDRVMSYLNAS 253


RESULT 5
US-08-684-687-4
; Sequence 4, Application US/08684687
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  253 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-684-687-4

  Query Match             88.0%;  Score 875;  DB 2;  Length 253;
  Best Local Similarity   86.8%;  Pred. No. 2.2e-92;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db         57 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 116

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||| ||||| ||| | |||||||| | |||  ||||||||||||||:||| ||
Db        117 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 176

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||  ||||:|||||| ||||||||||||||||||||||||||||
Db        177 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 236

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        237 RIRAVTIDRVMSYLNAS 253


RESULT 6
US-08-965-688-4
; Sequence 4, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  253 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-965-688-4

  Query Match             88.0%;  Score 875;  DB 2;  Length 253;
  Best Local Similarity   86.8%;  Pred. No. 2.2e-92;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db         57 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 116

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||| ||||| ||| | ||||||||| | |||  ||||||||||||||:||| ||
Db        117 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 176

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        177 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 236

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        237 RIRAVTIDRVMSYLNAS 253


RESULT 7
US-09-260-173-4
; Sequence 4, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
;             STREET: Spring House Corporate Center, PO Box 457
;             CITY: Spring House
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/260,173
;             FILING DATE: 01-Mar-1999
;             CLASSIFICATION: <Unknown>
;                             17-JUN-1994
;                             18-APR-1994
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/965,688
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/265,087
;             FILING DATE: 17-JUN-1994
;             APPLICATION NUMBER: US 08/229,282
;             FILING DATE: 18-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: WST51AUSA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-540-9206
;             TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 253 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-260-173-4

  Query Match             88.0%;  Score 875;  DB 4;  Length 253;
  Best Local Similarity   86.8%;  Pred. No. 2.2e-92;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db         57 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 116

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||| ||||| ||| | ||||||||| | |||  ||||||||||||||:||| ||
Db        117 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 176

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        177 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 236

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        237 RIRAVTIDRVMSYLNAS 253


RESULT 8
US-08-751-767A-2
; Sequence 2, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-2

  Query Match             87.4%;  Score 869;  DB 2;  Length 219;
  Best Local Similarity   86.3%;  Pred. No. 8.5e-92;
  Matches  170;  Conservative    8;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db         23 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 82

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||| ||||| ||| | |||||||| | ||| |||||||||||||:||| ||
Db         83 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 142

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        143 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 202

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||: ||||:|
Db        203 RIRAVTIDRVTSYLNAS 219


RESULT 9
US-08-751-767A-12
; Sequence 12, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  519 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-12

  Query Match             87.3%;  Score 868;  DB 2;  Length 519;
  Best Local Similarity   86.3%;  Pred. No. 4.2e-91;
  Matches  170;  Conservative    8;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db        323 RNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 382

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||| ||||| ||| | |||||||| | ||| |||||||||||||:||| ||
Db        383 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 442

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        443 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 502

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||: ||||:|
Db        503 RIRAVTIDRVTSYLNAS 519


RESULT 10
US-08-751-767A-8
; Sequence 8, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-8

  Query Match             87.3%;  Score 868;  DB 2;  Length 540;
  Best Local Similarity   86.3%;  Pred. No. 4.5e-91;
  Matches  170;  Conservative    8;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:|||||||||||| |||||||| | ||||||||||||||||||
Db        344 RNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 403
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Qy          61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
               ||||||||| ||||| ||| | ||||||||| | |||  |||||||||||||:||| ||
Db         404 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 463

Qy         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
               ||||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||
Db         464 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 523

Qy         181 RIRAVTIDRMMSYLNSS 197
               |||||||||: ||||:|
Db         524 RIRAVTIDRVTSYLNAS 540


RESULT 11
US-08-751-767A-10
; Sequence 10, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-10

  Query Match             87.3%;  Score 868;  DB 2;  Length 540;
  Best Local Similarity   86.3%;  Pred. No. 4.5e-91;
  Matches  170;  Conservative    8;  Mismatches   19;  Indels    0;  Gaps    0;

Qy           1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
               |:|| |:| ||:| ||:|||||||||| |||||||| | ||||||||||||||||||
Db         344 RNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 403

Qy          61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
               ||||||||| ||||| ||| | ||||||||| | |||  |||||||||||||:||| ||
Db         404 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 463

Qy         121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
               ||||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||
Db         464 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 523

Qy         181 RIRAVTIDRMMSYLNSS 197
               |||||||||: ||||:|
Db         524 RIRAVTIDRVTSYLNAS 540


RESULT 12
US-08-385-335A-12
; Sequence 12, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  215 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-385-335A-12

  Query Match             55.6%;  Score 553;  DB 2;  Length 215;
  Best Local Similarity   56.8%;  Pred. No. 1.6e-55;
  Matches  111;  Conservative   30;  Mismatches   55;  Indels    0;  Gaps    0;

Qy           2 SLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVE 61
               ||    | |  :||: |:|||:   : :: ||: |: ||||:|:|||||||:|:|||::
Db          20 SLARVIPVSGPARCLSQSRNLLKTTDDMVKTAREKLKHYSCTAEDIDHEDITRDQTSTLK 79

Qy          62 ACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNA 121
               ||||||  ||||||:|| |  | ||||   | | |  ||| |||||||||| ||:|:||
Db          80 TCLPLELHKNESCLATRETSSTTRGSCLPPQKTSLMMTLCLGSIYEDLKMYQTEFQAINA 139

Qy         122 KLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFR 181
               |      :|| ||: || |||||:|:|| |  |: ||  : | | |: |:|||||||||
Db         140 ALQNHNHQQIILDKGMLVAIDELMQSLNHNGETLRQKPPVGEADPYRVKMKLCILLHAFS 199

Qy         182 IRAVTIDRMMSYLNSS 197
               | |||:|:| ||:|:
Db         200 TRVVTINRVMGYLSSA 215


RESULT 13
US-08-659-206A-2
; Sequence 2, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 215 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-2

  Query Match             55.6%;  Score 553;  DB 2;  Length 215;
  Best Local Similarity   56.6%;  Pred. No. 1.6e-55;
  Matches  111;  Conservative   30;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          2 SLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVE 61
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Db         20 SLARVIPVSGPARCLSQSRNLLKTTDDMVKTAREKLKHYSCTAEDIDHEDITRDQTSTLK 79

Qy         62 ACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNA 121
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Qy        122 KLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFR 181
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Qy        182 IRAVTIDRMMSYLNSS 197
               | |||:|:| ||:|:
Db        200 TRVVTINRVMGYLSSA 215


RESULT 14
US-08-659-206A-5
; Sequence 5, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 215 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-5

  Query Match             55.6%;  Score 553;  DB 2;  Length 215;
  Best Local Similarity   56.6%;  Pred. No. 1.6e-55;
  Matches  111;  Conservative   30;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          2 SLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVE 61
              ||    |  |  :||: |:|||:   : :: ||: |: ||||:|:|||||||:|:|||::
Db         20 SLARVIPVSGPARCLSQSRNLLKTTDDMVKTAREKLKHYSCTAEDIDHEDITRDQTSTLK 79

Qy         62 ACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNA 121
               ||||||  ||||||:|| |  | ||||   | | |  ||| ||||||||||| ||:|:||
Db         80 TCLPLELHKNESCLATRETSSTTRGSCLPPQKTSLMMTLCLGSIYEDLKMYQTEFQAINA 139

Qy        122 KLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFR 181
                 |     :|| ||: || ||||||:|:|| |  |: ||  : | | |: |:|||||||||
Db        140 ALQNHNHQQIILDKGMLVAIDELMQSLNHNGETLRQKPPVGEADPYRVKMKLCILLHAFS 199

Qy        182 IRAVTIDRMMSYLNSS 197
               | |||:|:| ||:|:
Db        200 TRVVTINRVMGYLSSA 215


RESULT 15
US-08-328-254-6
; Sequence 6, Application US/08328254
; Patent No. 5710022
;  GENERAL INFORMATION:
;    APPLICANT:  Zhu, Xueliang
;    APPLICANT:  Lee, Wen-Hwa
;    TITLE OF INVENTION:  A No. 5710022el Nuclear Mitotic Phosphoprotein
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,254
;      FILING DATE:  24-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,239
;      FILING DATE:  22-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1191
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
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;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2482 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-328-254-6

  Query Match             8.5%;  Score 84.5;  DB 1;  Length 2482;
  Best Local Similarity   20.7%;  Pred. No. 4.4;
  Matches   39;  Conservative   43;  Mismatches   77;  Indels   29;  Gaps    7;

Qy         18 HSQNLLRAVSNTLQKARQTLELYSCTSEEIDHE--DITKDKTSTVEACLPLELTMNESCL 75
              | |  |:    :|:|  | | |  |   |::::   : |:|   |:    |:  ::||
Db       1400 HLQEKLQ----SLEKDSQALSLTKC---ELENQIAQLNKEKELLVKESESLQARLSESDY 1452

Qy         76 ASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFL-- 133
               :|    : :  |: :    | |||  |::   :   : :  ::  | |:|: :
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Qy        134 --------DQNMLTAIDELLQAL-----NFNSVTVPQKSSLEEPDFYKTKI-KLCILLHA 179
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Qy        180 FRIRAVTI 187
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Db       1569 FELDLVTL 1576


Search completed: July 15, 2003, 11:09:59
Job time : 7.7575 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 11:03:04 ; Search time 9.19771 Seconds
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2493.521 Million cell updates/sec

Title: US-09-917-265-50
Perfect score: 994
Sequence: 1 RSLPTASPSPGIFQCLNHSQ.....HAFRIRAVTIDRMMSYLNSS 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	994	100.0	197	10	US-09-917-265-50	Sequence 50, Appl
2	994	100.0	222	10	US-09-917-265-47	Sequence 47, Appl
3	994	100.0	222	10	US-09-917-265-105	Sequence 105, App
4	969	97.5	511	10	US-09-917-265-67	Sequence 67, Appl
5	969	97.5	533	10	US-09-917-265-62	Sequence 62, Appl
6	932	93.8	197	12	US-10-079-616-4	Sequence 4, Appli
7	932	93.8	222	12	US-10-079-616-3	Sequence 3, Appli
8	929	93.5	197	10	US-09-917-265-36	Sequence 36, Appl
9	929	93.5	222	10	US-09-917-265-33	Sequence 33, Appl
10	929	93.5	511	10	US-09-917-265-44	Sequence 44, Appl
11	929	93.5	533	10	US-09-917-265-39	Sequence 39, Appl
12	889	89.4	187	10	US-09-917-265-102	Sequence 102, App
13	875	88.0	253	10	US-09-924-703-6	Sequence 6, Appli
14	875	88.0	503	9	US-09-920-262A-9	Sequence 9, Appli
15	875	88.0	527	10	US-09-828-825-2	Sequence 2, Appli
16	875	88.0	537	10	US-09-828-825-8	Sequence 8, Appli
17	875	88.0	537	10	US-09-828-825-16	Sequence 16, Appl
18	875	88.0	542	10	US-09-828-825-6	Sequence 6, Appli
19	875	88.0	542	10	US-09-828-825-14	Sequence 14, Appl
20	875	88.0	547	10	US-09-828-825-10	Sequence 10, Appl
21	875	88.0	547	10	US-09-828-825-12	Sequence 12, Appl
22	871	87.6	526	10	US-09-828-825-4	Sequence 4, Appli
23	869	87.4	219	9	US-10-172-399-6	Sequence 6, Appli
24	869	87.4	219	10	US-09-754-014-5	Sequence 5, Appli
25	869	87.4	219	10	US-09-836-866-3	Sequence 3, Appli
26	553	55.6	215	9	US-10-172-399-2	Sequence 2, Appli
27	109	11.0	21	12	US-10-079-616-20	Sequence 20, Appl
28	89	9.0	539	9	US-10-028-072-140	Sequence 140, App
29	89	9.0	539	9	US-10-121-049-140	Sequence 140, App
30	89	9.0	539	9	US-10-123-904-140	Sequence 140, App
31	89	9.0	539	9	US-10-140-470-140	Sequence 140, App
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34	89	9.0	539	9	US-10-176-921-140	Sequence 140, App
35	89	9.0	539	9	US-10-137-865-140	Sequence 140, App
36	89	9.0	539	9	US-10-140-474-140	Sequence 140, App
37	89	9.0	539	9	US-10-142-431-140	Sequence 140, App
38	89	9.0	539	9	US-10-143-114-140	Sequence 140, App
39	89	9.0	539	9	US-10-140-002-140	Sequence 140, App
40	89	9.0	539	9	US-10-142-419-140	Sequence 140, App
41	89	9.0	539	9	US-10-152-031-4	Sequence 4, Appli
42	89	9.0	539	9	US-10-123-262-140	Sequence 140, App
43	89	9.0	539	9	US-10-142-423-140	Sequence 140, App
44	89	9.0	539	9	US-10-121-050-140	Sequence 140, App
45	89	9.0	539	9	US-10-141-755-140	Sequence 140, App

ALIGNMENTS

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RESULT 1
US-09-917-265-50
; Sequence 50, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-50

  Query Match             100.0%;  Score 994;  DB 10;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-92;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
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Db          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
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RESULT 2
US-09-917-265-47
; Sequence 47, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 222
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-47

  Query Match            100.0%;  Score 994;  DB 10;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 6.2e-92;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
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Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 3
US-09-917-265-105
; Sequence 105, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
;   LENGTH: 222
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-105

  Query Match            100.0%;  Score 994;  DB 10;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 6.2e-92;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         26 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
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Db         86 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||||||||||
Db        206 RIRAVTIDRMMSYLNSS 222


RESULT 4
US-09-917-265-67
; Sequence 67, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-67

  Query Match            97.5%;  Score 969;  DB 10;  Length 511;
  Best Local Similarity  97.0%;  Pred. No. 6.1e-89;
  Matches  191;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        315 RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 374

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 434

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 494

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:|||||||||
Db        495 RIRAVTINRMMSYLNSS 511


RESULT 5
US-09-917-265-62
; Sequence 62, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-62
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  Query Match           97.5%;  Score 969;  DB 10;  Length 533;
  Best Local Similarity  97.0%;  Pred. No. 6.4e-89;
  Matches  191;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        337 RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 396

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 456

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 516

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:|||||||||
Db        517 RIRAVTINRMMSYLNSS 533


RESULT 6
US-10-079-616-4
; Sequence 4, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 197 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-079-616-4
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  Query Match           93.8%;  Score 932;  DB 12;  Length 197;
  Best Local Similarity  92.9%;  Pred. No. 8.8e-86;
  Matches  183;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db          1 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 60

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||||||||||||||||||||||||||| | |||| |||||||||||||:||||||
Db         61 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 120

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 180

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:|||||||||
Db        181 RIRAVTINRMMSYLNSS 197


RESULT 7
US-10-079-616-3
; Sequence 3, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 222 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-079-616-3
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  Query Match             93.8%;  Score 932;  DB 12;  Length 222;
  Best Local Similarity   92.9%;  Pred. No. 1e-85;
  Matches  183;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db         26 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||||||||||||||||||||||| | |||| ||||||||||||||:||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:||||||||
Db        206 RIRAVTINRMMSYLNSS 222


RESULT 8
US-09-917-265-36
; Sequence 36, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-36

  Query Match             93.5%;  Score 929;  DB 10;  Length 197;
  Best Local Similarity   92.4%;  Pred. No. 1.8e-85;
  Matches  182;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db          1 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 60

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||||||||||||||||||||||| | |||| ||||||||||||||:||||||
Db         61 EACLPLELTMNESCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 120

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 180

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:||||||||
Db        181 RIRAVTINRMMSYLNAS 197


RESULT 9
US-09-917-265-33
; Sequence 33, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 222
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-33

  Query Match             93.5%;  Score 929;  DB 10;  Length 222;
  Best Local Similarity   92.4%;  Pred. No. 2.1e-85;
  Matches  182;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db         26 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 85

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||||||||||||||||||||||| | |||| ||||||||||||||:||||||
Db         86 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 145

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        146 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 205

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:||||||||
Db        206 RIRAVTINRMMSYLNAS 222


RESULT 10
US-09-917-265-44
; Sequence 44, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-44

  Query Match             93.5%;  Score 929;  DB 10;  Length 511;
  Best Local Similarity   92.4%;  Pred. No. 6.3e-85;
  Matches  182;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db        315 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 374

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||||||||||||||||||||||| | |||| ||||||||||||||:||||||
Db        375 EACLPLELTMNESCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 434

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        435 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 494

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:||||||||
Db        495 RIRAVTINRMMSYLNAS 511
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```
RESULT 11
US-09-917-265-39
; Sequence 39, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-39

  Query Match             93.5%;  Score 929;  DB 10;  Length 533;
  Best Local Similarity   92.4%;  Pred. No. 6.7e-85;
  Matches  182;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:||| :||||:|||||||| ||||:|||||||||||| ||||||||||||||||||||
Db        337 RNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTV 396

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              |||||||||||||||||||||||||||||| | |||| |||||||||||||:||||||
Db        397 EACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMN 456

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Db        457 AKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAF 516

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||:||||||:|
Db        517 RIRAVTINRMMSYLNAS 533


RESULT 12
US-09-917-265-102
; Sequence 102, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
;   LENGTH: 187
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-102

  Query Match             89.4%;  Score 889;  DB 10;  Length 187;
  Best Local Similarity   93.6%;  Pred. No. 1.7e-81;
  Matches  175;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         11 GIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTM 70
              |:|||||||| ||||:|||||||||||| ||||||||||||||||||||||||||||||
Db          1 GMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTM 60

Qy         71 NESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQ 130
              |||||||||||||||||||| | |||| |||||||||||||:||||||||||||||||
Db         61 NESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQ 120

Qy        131 IFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRM 190
              |||||||||||||||||| ||||||| |||||||||||||||||||||||||||:||
Db        121 IFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRM 180

Qy        191 MSYLNSS 197
              |||||:|
Db        181 MSYLNAS 187


RESULT 13
US-09-924-703-6
; Sequence 6, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic amino
;   OTHER INFORMATION: acid sequence of the 30 kD subunit of NKSF
US-09-924-703-6

  Query Match             88.0%;  Score 875;  DB 10;  Length 253;
  Best Local Similarity   86.8%;  Pred. No. 6.5e-80;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
              |:|| |:| ||:| ||:||||||||||| ||||||||| | ||||||||||||||||||
Db         57 RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTV 116

Qy         61 EACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMN 120
              ||||||||| ||||| ||| | ||||||||| | |||  ||||||||||||||:||| ||
Db        117 EACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMN 176

Qy        121 AKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAF 180
              |||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        177 AKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF 236

Qy        181 RIRAVTIDRMMSYLNSS 197
              |||||||||:|||||:|
Db        237 RIRAVTIDRVMSYLNAS 253


RESULT 14
```

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US-09-920-262A-9
; Sequence 9, Application US/09920262A
; Publication No. US20030124123A1
; GENERAL INFORMATION:
;  APPLICANT: Shealy, David
;  APPLICANT:  Knight, David
;  APPLICANT:  Scallon, Bernie
;  APPLICANT:  Giles-Komar, Jill
;  APPLICANT:  Peritt, David
;  TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
;  FILE REFERENCE: CEN0248
;  CURRENT APPLICATION NUMBER: US/09/920,262A
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 60/223,358
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 60/236,827
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 9
;   LENGTH: 503
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-920-262A-9

  Query Match             88.0%;  Score 875;  DB 9;  Length 503;
  Best Local Similarity   86.8%;  Pred. No. 1.6e-79;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 RSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTV 60
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RESULT 15
US-09-828-825-2
; Sequence 2, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 527
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-09-828-825-2

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  Best Local Similarity   86.8%;  Pred. No. 1.7e-79;
  Matches  171;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

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Search completed: July 15, 2003, 11:11:43
Job time : 10.1977 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:27:32 ; Search time 2608.93 Seconds
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Title: US-09-917-265-52
Perfect score: 921
Sequence: 1 atatgggaactggagaaaga.....gggcatctgtgtcctgcagt 921

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	921	100.0	990	6	E15017	E15017 Canine mRNA
3	917.8	99.7	1015	4	CFU49100	U49100 Canis famil
4	914.6	99.3	990	6	AR151061	AR151061 Sequence
5	825	89.6	1006	4	FCIL12P40	Y07762 F.catus mRN
6	823.4	89.4	990	4	FCU83184	U83184 Felis catus
7	823.4	89.4	990	6	AX076200	AX076200 Sequence
8	823.4	89.4	990	6	AX076482	AX076482 Sequence
9	823.4	89.4	4522	6	AX076209	AX076209 Sequence
10	823.4	89.4	4522	6	AX076476	AX076476 Sequence
11	778.6	84.5	990	6	AX154603	AX154603 Sequence
12	761	82.6	1058	4	ECIL12P40	Y11129 Equus cabal
13	759.4	82.5	1626	12	AF401989	AF401989 Synthetic
14	737.4	80.1	984	6	AX154599	AX154599 Sequence
15	735.8	79.9	984	6	AX154600	AX154600 Sequence
16	724.2	78.6	987	6	AR008950	AR008950 Sequence
17	724.2	78.6	987	6	AX154633	AX154633 Sequence
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20	724.2	78.6	987	6	I28591	I28591 Sequence 1
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42	707	76.8	1012	4	BTU11815	U11815 Bos taurus
43	707	76.8	1019	6	E35794	E35794 Process for
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ALIGNMENTS

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LOCUS AR151071 990 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6231850.
ACCESSION AR151071
VERSION AR151071.1 GI:15117121
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 990)
AUTHORS Okano,F., Satoh,M. and Yamada,K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
FEATURES Location/Qualifiers

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  Best Local Similarity  100.0%;  Pred. No. 5e-251;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
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LOCUS       E15017                   990 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 40kDa subunit,complete cds.
ACCESSION   E15017
VERSION     E15017.1  GI:5709700
KEYWORDS    JP 1998036397-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 1 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/1
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
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            CC   topology: Linear;
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FEATURES             Location/Qualifiers
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  Query Match            100.0%;  Score 921;  DB 6;  Length 990;
  Best Local Similarity  100.0%;  Pred. No. 5e-251;
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Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db        967 TGGGCATCTGTGTCCTGCAGT 987
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DEFINITION  Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U49100
VERSION     U49100.1  GI:1223907
KEYWORDS    .
SOURCE      Canis familiaris.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
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                     LIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCV
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                     QAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCS"
BASE COUNT      285 a    251 c    254 g    225 t
ORIGIN

  Query Match           99.7%;  Score 917.8;  DB 4;  Length 1015;
  Best Local Similarity  99.8%;  Pred. No. 4.1e-250;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAAGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCGTACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db        967 TGGGCATCTGTGTCCTGCAGT 987
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RESULT 4
AR151061
LOCUS       AR151061                990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6231850.
ACCESSION   AR151061
VERSION     AR151061.1  GI:15117111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
BASE COUNT      278 a    243 c    251 g    218 t
ORIGIN

  Query Match           99.3%;  Score 914.6;  DB 6;  Length 990;
  Best Local Similarity   99.6%;  Pred. No. 3.3e-249;
  Matches  917;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
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Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        967 TGGGCATCTGTGCCCTGCAGT 987


RESULT 5
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 13-MAY-1997
DEFINITION  F.catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      cat.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 1006)
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  MEDLINE   97246745
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1006
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .990
                     /gene="IL-12.p40"
     CDS             1. .990
                     /gene="IL-12.p40"
                     /note="heterodimer with IL-12 p35 chain"
                     /codon_start=1
                     /product="interleukin-12 p40 chain"
                     /protein_id="CAA69068.1"
                     /db_xref="GI:2102665"
                     /db_xref="SWISS-PROT:O02744"
                     /translation="MHPQQLVIAWLSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
BASE COUNT      288 a    258 c    249 g    211 t
ORIGIN

  Query Match           89.6%;  Score 825;  DB 4;  Length 1006;
  Best Local Similarity   93.5%;  Pred. No. 1.1e-223;
  Matches  861;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921

Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 6
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  MEDLINE   98182592
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCDTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
BASE COUNT      283 a    251 c    249 g    207 t
ORIGIN

  Query Match             89.4%;  Score 823.4;  DB 4;  Length 990;
  Best Local Similarity   93.4%;  Pred. No. 3.1e-223;
  Matches  860;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Db        127 GGAGAAATGGTGGTCCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||| |||||||||||| |||||||||  ||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || |||||||||| |||||||||||| ||||| || |||||||||||| ||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||| ||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 7
AX076200
LOCUS       AX076200                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p40"
BASE COUNT      283 a    249 c    248 g    210 t
ORIGIN

  Query Match           89.4%;  Score 823.4;  DB 6;  Length 990;
  Best Local Similarity   93.4%;  Pred. No. 3.1e-223;
  Matches  860;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||| |||||| |||| ||||||||||||||||||| ||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
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Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
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Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
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Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
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Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 8
AX076482
LOCUS       AX076482                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
BASE COUNT      283 a    249 c    248 g    210 t
ORIGIN
```

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  Query Match             89.4%;  Score 823.4;  DB 6;  Length 990;
  Best Local Similarity   93.4%;  Pred. No. 3.1e-223;
  Matches  860;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
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Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
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Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
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Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
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Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
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Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 9
AX076209
LOCUS       AX076209               4522 bp    DNA     linear   PAT 06-FEB-2001

DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4522)
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
BASE COUNT     1180 a   1126 c   1106 g   1110 t
ORIGIN

  Query Match             89.4%;  Score 823.4;  DB 6;  Length 4522;
  Best Local Similarity   93.4%;  Pred. No. 3.6e-223;
  Matches  860;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
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Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
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Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
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Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
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Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
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Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
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Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

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Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db       4013 TGGGCATCCGTGTCCTGCAGT 4033


RESULT 10
AX076476
LOCUS       AX076476               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4522)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
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BASE COUNT     1180 a   1126 c   1106 g   1110 t
ORIGIN

  Query Match            89.4%;  Score 823.4;  DB 6;  Length 4522;
  Best Local Similarity  93.4%;  Pred. No. 3.6e-223;
  Matches  860;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
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Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
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Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
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Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
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Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
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Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| |||||||||| |||||| |||||||||| ||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
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Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
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Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||| | |||||||||||||| |||||||||||| ||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db       4013 TGGGCATCCGTGTCCTGCAGT 4033


RESULT 11
AX154603
LOCUS       AX154603               990 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 7 from Patent WO0140257.
ACCESSION   AX154603
VERSION     AX154603.1  GI:14536186
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 7 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      270 a    250 c    254 g    216 t
ORIGIN

  Query Match            84.5%;  Score 778.6;  DB 6;  Length 990;
  Best Local Similarity  90.3%;  Pred. No. 1.8e-210;
  Matches  832;  Conservative    0;  Mismatches   89;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAATTGGACTGGTACCCGGATGCCCCT 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||| ||||  | || |||||||||||||| |||||| |||||||||
Db        127 GGAGAAATGGTGGTCCTCGCCTGTGACACTCCTGAAGAAGATGGCATCACCTGGACCTCA 186
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Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||| ||| | ||  |||| ||||| |||||||||| ||||||||  |||
Db        187 GACCAGAGCAGTGAGGTCTTGGGCACTGGCAAAACCCTGACCATCCACGTCAAAGAGTTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||| ||||| |  |||||||||   |||||||||  |||||||||
Db        247 GGAGATGCTGGCCAGTACACCTGTCGCAAAGGAGGCGCAGTTCTGAGCCAGTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
               || |||||||||| ||||||||||||||||||||||||||| ||||| || ||||||||
Db        307 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAAGACCAGAAAGAG 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||  |||||||||||||||||||||||||||||||| || ||||||||||| |||
Db        367 CCCAAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||| |||||||||| |||||||||||| |||||||| |||||||||| |
Db        427 TGGTGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||| |||||||| || |||| || ||||||||||||||  ||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCCGTTACACTCTCTGCAGAGAGGGTCAGCATG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||| ||||||| |||| |||||||||||||||||||||||||||||||||||||||||
Db        547 GACCACAGGGAGTATAACAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||||||||||||||||| ||||||||||  ||| ||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCTGACCCACCCAAGAACTTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||| |||||||| |||||||||| ||||| ||||||
Db        727 CAGCTGAAGCCATTAAAGAATTCTCGACACGTGGAGATCAGCTGGGAGTACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||| |||||||||||||||| |||||||  ||| |  | || |  ||||||||||||
Db        787 TGGAGCATCCCACATTCCTACTTTTCCCTGATGTTTGGTGTTCAAGTTCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        847 AAGAGAGAAAAGAAAGATAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||| |||||||||||| || ||||| ||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTACAGCTCATCTTGGAGCGAA 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        967 TGGGCATCTGTGCCCTGCAGT 987


RESULT 12
ECIL12P40
LOCUS       ECIL12P40               1058 bp    mRNA    linear   MAM 17-NOV-1999
DEFINITION  Equus caballus mRNA for interleukin 12 p40 subunit.
ACCESSION   Y11129
VERSION     Y11129.1  GI:5441622
KEYWORDS    interleukin-12 p40.
SOURCE      Equus caballus.
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 1058)
  AUTHORS   Nicolson,L., Penha-Goncalves,M.N., Keanie,J.L., Logan,N.A.,
            Argyle,D.J. and Onions,D.E.
  TITLE     Cloning and sequencing of horse interleukin-12 and interleukin-18
            cDNAs
  JOURNAL   Immunogenetics 50 (1-2), 94-97 (1999)
  MEDLINE   20009534
   PUBMED   10541814
REFERENCE   2  (bases 1 to 1058)
  AUTHORS   Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-FEB-1997) L. Nicolson, Dept. of Vet. Pathology,
            University of Glasgow Vet. School, Bearsden Rd., Glasgow G61 1QH,
            UK
FEATURES             Location/Qualifiers
     source          1. .1058
                     /organism="Equus caballus"
                     /db_xref="taxon:9796"
                     /cell_line="LPS-stimulated alveolar macrophages"
                     /cell_type="alveolar macrophages"
     gene            1. .990
                     /gene="IL-12 p40"
     CDS             1. .990
                     /gene="IL-12 p40"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit"
                     /protein_id="CAA72011.1"
                     /db_xref="GI:5441623"
                     /translation="MCHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
                     MVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHL
                     LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                     LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
                     QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCS"
     sig_peptide     1. .66
                     /gene="IL-12 p40"
     misc_feature    1. .12
                     /gene="IL-12 p40"
                     /note="primer-derived sequence"
     variation       714
                     /gene="IL-12 p40"
                     /note="allelic difference, no change in amino acid
                     sequence"
                     /replace="g"
     misc_feature    1041. .1058
                     /note="primer-derived sequence"
BASE COUNT      284 a    269 c    282 g    223 t
ORIGIN

  Query Match           82.6%;  Score 761;  DB 4;  Length 1058;
  Best Local Similarity   89.1%;  Pred. No. 1.9e-205;
  Matches  821;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||||||| |||||||||| ||||| ||| ||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTGTATGTTGTAGAATTGGATTGGTACCCTGATGCCCCT 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||| ||||||||||||||| | |||||| ||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACCCCTGAAGAAGAAGGCATCACCTGGACCTCG 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              || |||||||  ||| ||| |||| |||||  |||||  |||||||||||||||||| |||
Db        187 GCCCAGAGCAATGAGGTCTTAGGCTCTGGCAAAACCTTGACCATCCAAGTCAAAGAGTTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||  ||| ||||| || ||||||||| ||||||||||||  || | ||||
Db        247 GGAGATGCTGGCTGGTACACCTGTCACAAAGGAGGCGAGGTTCTGAGCCATTCTCACCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              || ||||||| || |||||||||||||||||||||||| || ||||| || |||||||||
Db        307 CTGCTTCACAAGAAGGAAGATGGAATTTGGTCCACTGACATTTTAAAAGACCAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||| ||||||  |||||||||||||||||||||||||| ||||||||||||||
Db        367 TCCAAAAATAAGACCTTTCTAAAATGTGAGGCAAAGAATTATTCCGGACGTTTCACATGC 426
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Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
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Db        427 TGGTGGCTGACAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGAGGTTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||| ||||||||| |||||||||| |||||| || |||||||||||||| |||
Db        487 TCTGACCCCCGAGGGGTGACGTGTGGAGCAGCGACACTCTCCGCAGAGAGGGTCAGCGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||| ||||||| |||||||||||||| |||||||||||||||||||||||||||||  |
Db        547 GACGACAGGGAGTATAAGAAGTACACGGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCC 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              |||||||||||||| ||||| ||| |||||||||||||| ||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTGCCCATTGAGATCGTGGTGGATGCTGTTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||| |||||||||||| |||||||||||||||||||||||  ||||||
Db        667 AACTACACCAGCGGCTTCTTCATCAGGGACATCATCAAACCAGACCCACCCAAGAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||| || |||||||||| |||||||||||||| |||||||| |||
Db        727 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCCGAGACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||||||||||| |  || |||| ||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTCTCTATTCAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |  |||| |||||| ||||||| | |||| |||| |||||||  |||   ||||||
Db        847 AAGAAGGAAAGGAAAGACAGACTCTTCATGGATGAGACTTCAGCCACAGTCACATGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||| | ||||||| || |||||| | |||||||||| || ||||||||||||||
Db        907 AAGGATGGCCAGATCCGTGTCCAAGCCAGGGACCGCTACTACAGCTCATCCTGGAGCGAA 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||| || |||||||||
Db        967 TGGGCATCCGTATCCTGCAGT 987


RESULT 13
AF401989
LOCUS       AF401989               1626 bp    mRNA    linear   SYN 14-FEB-2002
DEFINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION   AF401989
VERSION     AF401989.1  GI:18656516
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1626)
  AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
            Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
            Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
  MEDLINE   21626920
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
     source          1. .1626
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     CDS             1. .1626
                     /note="derived from Equus caballus; N-terminal p40 subunit
                     linked by (Gly4Ser)3 linker to signal-peptide deleted p35
                     subunit"
                     /codon_start=1
                     /transl_table=11
                     /product="single chain interleukin-12"
                     /protein_id="AAL77817.1"
                     /db_xref="GI:18656517"
                     /translation="MGHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
                     MVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHL
                     LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                     LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
                     QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCSGGGGS
                     GGGGSGGGGSRNLPTATPGPGMFQCLNHSQNLLRTVSNTLQKARQTLEFYSCTSEEID
                     HEDITKDKSSTVAACLPLELAPNESCLASREISFITNGSCLTPGKASSMMTLCLSSIY
                     EDLKMYQVEFKAMNAKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETVPQKPSLEGL
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     primer_bind     1. .14
     misc_feature    15. .987
                     /note="interleukin-12 p40 sequence"
     misc_feature    988. .1032
                     /note="linker"
     misc_feature    1033. .1611
                     /note="interleukin-12 p35 sequence"
     primer_bind     complement(1612. .1626)
BASE COUNT      429 a    425 c    427 g    345 t
ORIGIN

  Query Match           82.5%;  Score 759.4;  DB 12;  Length 1626;
  Best Local Similarity  89.0%;  Pred. No. 5.5e-205;
  Matches  820;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAGATGTGTATGTTGTAGAATTGGATTGGTACCCTGATGCCCCT 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACCCCTGAAGAAGAAGGCATCACCTGGACCTCG 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              || ||||||| ||| ||| |||| ||||| |||||  |||||||||||||||||| |||
Db        187 GCCCAGAGCAATGAGGTCTTAGGCTCTGGCAAAACCTTGACCATCCAAGTCAAAGAGTTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||  ||| ||||| || |||||||| ||||||||||||  || | ||||
Db        247 GGAGATGCTGGCTGGTACACCTGTCACAAAGGAGGCGAGGTTCTGAGCCATTCTCACCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              || ||||||| || |||||||||||||||||||||| || ||||| || ||||||||
Db        307 CTGCTTCACAAGAAGGAAGATGGAATTTGGTCCACTGACATTTTAAAAGACCAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||| |||||| |||||||||||||||||||||| ||||||||||||||
Db        367 TCCAAAAATAAGACCTTTCTAAAATGTGAGGCAAAGAATTATTCCGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||| |||||||||||||||||||||||||||||||||||| |||||||| | |
Db        427 TGGTGGCTGACAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGAGGTTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||| |||||||||| |||||||||| |||||| || |||||||||||||| |||
Db        487 TCTGACCCCCGAGGGGTGACGTGTGGAGCAGCGACACTCTCCGCAGAGAGGGTCAGCGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||| ||||||| |||||||||||||| |||||||||||||||||||||||||||||  |
Db        547 GACGACAGGGAGTATAAGAAGTACACGGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCC 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              |||||||||||||| ||||| ||| |||||||||||||| |||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTGCCCATTGAGATCGTGGTGGATGCTGTTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
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Db        667 AACTACACCAGCGGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Db        727 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCCGAGACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTCTCTATTCAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        847 AAGAAGGAAAGGAAAGACAGACTCTTCATGGATGAGACTTCAGCCACAGTCACATGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Db        907 AAGGATGGCCAGATCCGTGTCCAAGCCAGGGACCGCTACTACAGCTCATCCTGGAGCGAA 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921

Db        967 TGGGCATCCGTATCCTGCAGT 987


RESULT 14
AX154599
LOCUS       AX154599                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3 from Patent WO0140257.
ACCESSION   AX154599
VERSION     AX154599.1  GI:14536182
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 3 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      267 a    246 c    254 g    217 t
ORIGIN

  Query Match            80.1%;  Score 737.4;  DB 6;  Length 984;
  Best Local Similarity  88.4%;  Pred. No. 9.7e-199;
  Matches  814;  Conservative    0;  Mismatches  101;  Indels    6;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Db         67 ATATGGGAACTGGAGAAAAATGTTTATGTTGTAGAATTGGATTGGTACCCGGATGCCCCT 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Db        127 GGAGAAATGGTGGTCCTCGCCTGTGACACTCCTGAAGAAGATGGCATCACCTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Db        187 GACCAGAGCAGTGGGGTCTTGGGCACTGGCAAAACCCTGACCATCCACGTCAAAGAGTTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Db        247 GGAGATGCTGGCCAGTACACCTGTCGCAAAGGAGGCGCAGTTCTGAGCCAGTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Db        307 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Db        367 CCCAAAGCTAAGAGTTTTTTAAAATGTGAGGCAAAGGATTATTCTGGACACTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Db        427 TGGTGGCTGACAACAATCAGTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCCGTTACACTCTCTGCAGAGAGGGTCAGCATG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Db        547 GACCACAGGGAGTATAACAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACTTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Db        727 CAGCTGAGACCACTAAAGAATTCTCGGCAGGTGGAGGTCAACTGGGAGTACCCTGACACG 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Db        787 TGGAGCACCCCACATTCCTACTTTTCCCTGACGTTTTGTGTTCAGGTCCAGGGAAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        847 AAGAGAGAAAAGAA------ACTCTTCATGGACCAAACCTCAGCCAAAGTCACATGCCAC 900

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Db        901 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTACAGCTCATCTTGGAGCGAA 960

Qy        901 TGGGCATCTGTGTCCTGCAGT 921

Db        961 TGGGCATCTGTGCCCTGCAGT 981


RESULT 15
AX154600
LOCUS       AX154600                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0140257.
ACCESSION   AX154600
VERSION     AX154600.1  GI:14536183
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 4 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
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BASE COUNT      272 a    254 c    247 g    211 t
ORIGIN

  Query Match            79.9%;  Score 735.8;  DB 6;  Length 984;
  Best Local Similarity  88.3%;  Pred. No. 2.8e-198;
  Matches  813;  Conservative    0;  Mismatches  102;  Indels    6;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Db         67 ATATGGGAACTGGAGAAAAATGTTTATGTTGTAGAATTGGATTGGTATCCTGATGCTCCT 126
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Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
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Db        127 GGAGAAACAGTGGTCCTCGCCTGTGACACTCCTGAAGAAGATGGCATCACCTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||| ||||| ||  |||| ||||| |||||||||| |||||||| |||
Db        187 GACCAGAGCAGTGAGGTCCTGGGCACTGGCAAAACCCTGACCATCCACGTCAAAGAGTTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
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Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||| |||||||||| |||||||||||| ||||||||| |||||||||| |
Db        427 TGGTGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||| |||||||| || ||||| || |||||||||||||  ||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCCGTTACACTCTCTGCAGAGAGGGTCAGCATG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||| |||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
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Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
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Db        667 AACTACACCAGCAGGTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACTTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || ||||  ||| | || |||||||| |||||||| |||||||||| ||||| ||||||
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Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || ||||||||||       ||||| | ||||| | |||||||||| |||   ||||||
Db        847 AAGAGAGAAAAGAA------ACTCTTCATGGACCAAACCTCAGCCAAAGTCACATGCCAC 900

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||| |||||||||| | || ||||| ||||||||
Db        901 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACCACAGCTCATCTTGGAGCGAA 960

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
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Search completed: July 16, 2003, 10:34:40
Job time : 2609.93 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 04:18:07 ; Search time 247.624 Seconds
(without alignments)
8375.975 Million cell updates/sec

Title: US-09-917-265-52
Perfect score: 921
Sequence: 1 atatgggaactggagaaaga.....gggcatctgtgtcctgcagt 921

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	921	100.0	990	19	AAV13817	Canine IL-12 P40 s
2	921	100.0	990	20	AAX35625	Nucleic acid encod
3	921	100.0	990	20	AAX03162	Nucleic acid encod
4	921	100.0	990	22	AAI64388	Canine coding sequ
5	917.8	99.7	990	19	AAV13816	Canine IL-12 P40 s
6	917.8	99.7	990	20	AAX35615	Nucleic acid encod
7	917.8	99.7	990	20	AAX03152	Nucleic acid encod
8	917.8	99.7	990	22	AAI64378	Canine coding sequ
9	896.8	97.4	924	20	AAX18177	Canine mature CLAF
10	896.8	97.4	2154	20	AAX18176	Canine full length
11	826.6	89.8	921	19	AAV56626	Feline FLAFp40 cDN
12	826.6	89.8	2193	19	AAV56625	Feline FLAFp40 cDN
13	825	89.6	921	19	AAV56627	Feline FLAFp40 cDN
14	823.4	89.4	990	22	AAF26082	Feline IL-12p40 en
15	823.4	89.4	990	22	AAF26085	Feline IL-12p40 en
16	823.4	89.4	4522	22	AAF26076	Feline IL-12p40 en
17	823.4	89.4	4522	22	AAF26094	Plasmid pMol-fil12
18	778.6	84.5	990	22	AAD15209	Modified human cyt
19	737.4	80.1	984	22	AAD15205	Modified human cyt
20	735.8	79.9	984	22	AAD15206	Modified human cyt
21	724.2	78.6	987	16	AAQ97484	Human interleukin-
22	724.2	78.6	987	19	AAV07273	Human Interleukin-
23	724.2	78.6	987	19	AAV07217	DNA encoding human
24	724.2	78.6	987	20	AAZ40404	Human interleukin
25	724.2	78.6	987	22	AAD15210	Human cytokine p40
26	724.2	78.6	1007	22	AAD18585	Human interleukin-
27	724.2	78.6	1018	15	AAQ67879	EPV 42 kD promoter
28	724.2	78.6	1018	20	AAZ08510	EPV 42 kDa/human I
29	724.2	78.6	1389	22	AAF76880	Human p40-IL-2 cod
30	724.2	78.6	1397	18	AAV00401	40 kDa subunit of
31	724.2	78.6	1397	18	AAT77849	40 kDa subunit of
32	724.2	78.6	1397	18	AAT97969	40 kDa subunit of
33	724.2	78.6	1397	19	AAV37767	Cytotoxic lymphocy
34	724.2	78.6	1399	21	AAZ40021	Human p40 coding s
35	724.2	78.6	2362	13	AAQ23586	Natural killer cel
36	724.2	78.6	2362	17	AAT48098	Human interleukin-
37	724.2	78.6	2362	19	AAV42535	Human interleukin-
38	724.2	78.6	2362	19	AAV15227	Heterodimeric huma
39	724.2	78.6	2362	21	AAZ28862	Human interleukin-
40	724.2	78.6	2362	22	AAF56280	IL-12 vaccine adju
41	724.2	78.6	5686	20	AAZ40415	Plasmid pIN1143 co
42	724.2	78.6	6139	21	AAZ40023	Interleukin-12 fus
43	722.6	78.5	987	20	AAV83199	Interleukin (IL)-1
44	722.6	78.5	2300	21	AAA92406	Human interleukin
45	722.6	78.5	8578	24	AAD31545	pIRES-hB7-1-IL12.1

ALIGNMENTS

RESULT 1
AAV13817
ID AAV13817 standard; cDNA to mRNA; 990 BP.
XX
AC AAV13817;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit cDNA.
XX
KW Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1..990
FT /*tag= a
FT /product= interleukin-12_P40_subunit
XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.

```
DR   P-PSDB; AAW41791.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 10; Pages 10-11; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

  Query Match            100.0%;  Score 921;  DB 19;  Length 990;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-276;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCTGTGTCCTGCAGT 987


RESULT 2
AAX35625
ID   AAX35625 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35625;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02342.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 14-15; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

  Query Match            100.0%;  Score 921;  DB 20;  Length 990;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-276;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

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Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
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Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
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Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy.       301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
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Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

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Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCTGTGTCCTGCAGT 987


RESULT 3
AAX03162
ID   AAX03162 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03162;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag= a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84373.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

  Query Match             100.0%;  Score 921;  DB 20;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-276;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
                    |||||||||||||||||||||
Db        967 TGGGCATCTGTGTCCTGCAGT 987


RESULT 4
AAI64388
ID   AAI64388 standard; DNA; 990 BP.
XX
AC   AAI64388;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1..66
FT                   /*tag=  b
FT   mat_peptide     67..987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66482.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Claim 6; Page 16-17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

  Query Match             100.0%;  Score 921;  DB 22;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-276;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCTGTGTCCTGCAGT 987


RESULT 5
AAV13816
ID   AAV13816 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13816;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag= a
FT                   /product= interleukin-12_P40_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41790.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 8; Page 8; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

  Query Match            99.7%;  Score 917.8;  DB 19;  Length 990;
  Best Local Similarity  99.8%;  Pred. No. 3.7e-275;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        967 TGGGCATCTGTGCCCTGCAGT 987


RESULT 6
AAX35615
ID   AAX35615 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35615;
XX
DT   09-JUL-1999  (first entry)
XX
```

```
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;    98JP-0133345.
XX
PR   07-AUG-1997;    97JP-0213755.
PR   16-MAY-1997;    97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02339.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 12; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

  Query Match             99.7%;  Score 917.8;  DB 20;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 3.7e-275;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        967 TGGGCATCTGTGCCCTGCAGT 987


RESULT 7
AAX03152
ID   AAX03152 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03152;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;    98WO-JP02031.
XX
PR   16-MAY-1997;    97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
```

```
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84371.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

  Query Match             99.7%;  Score 917.8;  DB 20;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 3.7e-275;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        967 TGGGCATCTGTGCCCTGCAGT 987


RESULT 8
AAI64378
ID   AAI64378 standard; DNA; 990 BP.
XX
AC   AAI64378;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1..66
FT                   /*tag=  b
FT   mat_peptide     67..987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66480.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Claim 6; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

  Query Match             99.7%;  Score 917.8;  DB 22;  Length 990;
```

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  Best Local Similarity   99.8%;  Pred. No. 3.7e-275;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        967 TGGGCATCTGTGCCCTGCAGT 987


RESULT 9
AAX18177
ID   AAX18177 standard; cDNA; 924 BP.
XX
AC   AAX18177;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74323.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 32; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 other;

  Query Match           97.4%;  Score 896.8;  DB 20;  Length 924;
  Best Local Similarity   98.9%;  Pred. No. 1.2e-268;
  Matches  914;  Conservative    0;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        241 TTGATTCAC---AAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAA 297
              ||   | |   |||||  ||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGATTCCACAAAAAAGAAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAA 300

Qy        298 GAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACA 360

Qy        358 TGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGC 417
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGC 420

Qy        418 TTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGA 477
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGA 480

Qy        478 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCC 537
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCC 540

Qy        538 TCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTAT 597
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTAT 600

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAAC 657
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAAC 660

Qy        658 CTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGAC 717
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGAC 720

Qy        718 ACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAG 777
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAG 780

Qy        778 AACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 837
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 840

Qy        838 CACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGC 897
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGC 900

Qy        898 GACTGGGCATCTGTGTCCTGCAGT 921
                |||||||||||||||||||||||||
Db        901 GACTGGGCATCTGTGTCCTGCAGT 924
```

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RESULT 10
AAX18176
ID   AAX18176 standard; cDNA; 2154 BP.
XX
AC   AAX18176;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74322.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 30-31; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 other;
```

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  Query Match             97.4%;  Score 896.8;  DB 20;  Length 2154;
  Best Local Similarity   98.9%;  Pred. No. 2e-268;
  Matches  914;  Conservative    0;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 177

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 237

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 297

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 357

Qy        241 TTGATTCAC---AAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAA 297
              ||   | |   |||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TTTGATTCCACAAAAAAGAAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAA 417

Qy        298 GAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACA 477

Qy        358 TGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGC 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 TGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGC 537

Qy        418 TTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGA 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 TTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGA 597

Qy        478 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCC 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCC 657

Qy        538 TCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTAT 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 TCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTAT 717

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAAC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 GAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAAC 777

Qy        658 CTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGAC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 CTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGAC 837

Qy        718 ACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAG 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 ACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAG 897

Qy        778 AACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 837
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 AACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 957

Qy        838 CACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGC 897
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 CACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGC 1017

Qy        898 GACTGGGCATCTGTGTCCTGCAGT 921
                |||||||||||||||||||||||||
Db       1018 GACTGGGCATCTGTGTCCTGCAGT 1041


RESULT 11
AAV56626
ID   AAV56626 standard; cDNA; 921 BP.
XX
AC   AAV56626;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #1.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 20; Page 55; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment
CC   of feline autoimmune diseases e.g. as caused by feline herpes virus
CC   or feline calcivirus.
XX
SQ   Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 other;

  Query Match             89.8%;  Score 826.6;  DB 19;  Length 921;
  Best Local Similarity   93.6%;  Pred. No. 9.1e-247;
  Matches  862;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||| |||| |||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              | ||||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| |||||||||| |||||| |||||||||| ||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||| |||||||||||||| ||||||||||  ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||| ||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| |||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||||| |||||||||||||||| |||||||||||  ||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||| ||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 12
AAV56625
ID   AAV56625 standard; cDNA; 2193 BP.
XX
AC   AAV56625;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             64..1053
FT                   /*tag=  a
FT   sig_peptide     64..129
FT                   /*tag=  b
```

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FT   mat_peptide      130..1050
FT                    /*tag=  c
FT                    /product= "FLAFp40"
FT                    /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76173.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 19; Page 52-54; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 other;

  Query Match             89.8%;  Score 826.6;  DB 19;  Length 2193;
  Best Local Similarity   93.6%;  Pred. No. 1.5e-246;
  Matches  862;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||| | |||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
               |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||| |||||||||||||| ||||||||| |||||||||| |
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||| |||||||||| |||||| |||||||||| ||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||

Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||| |||||||||||| |||||||||  ||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || |||||||||| |||||||||||| ||||| || |||||||||||| ||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              ||||||||| ||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 13
AAV56627
ID   AAV56627 standard; cDNA; 921 BP.
XX
AC   AAV56627;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #2.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 21; Page 56-57; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment
CC   of feline autoimmune diseases e.g. as caused by feline herpes virus
CC   or feline calcivirus.
```

```
XX
SQ   Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 other;

  Query Match            89.6%;  Score 825;  DB 19;  Length 921;
  Best Local Similarity   93.5%;  Pred. No. 2.9e-246;
  Matches  861;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              | ||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              |||| |||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||| |||||||||| |||||| |||||||||| |||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              |||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||| |||||||||||||| |||||||||  ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| |||||| ||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||| ||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 14
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AAF26082
ID   AAF26082 standard; DNA; 990 BP.
XX
AC   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter  -
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 other;

  Query Match            89.4%;  Score 823.4;  DB 22;  Length 990;
  Best Local Similarity   93.4%;  Pred. No. 9.5e-246;
  Matches  860;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||| |||||| |||| ||||||||||||||||||| ||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
```

```
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

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Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921

Db        967 TGGGCATCCGTGTCCTGCAGT 987
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RESULT 15
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
AC   AAF26085;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs -
XX
PS   Claim 3; Page 30; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 other;

  Query Match             89.4%;  Score 823.4;  DB 22;  Length 990;
  Best Local Similarity   93.4%;  Pred. No. 9.5e-246;
  Matches  860;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||| |||||||||| |||||| |||||||||| ||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987
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Search completed: July 16, 2003, 06:46:42
Job time : 249.624 secs

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:30:08 ; Search time 1669.03 Seconds
(without alignments)
8936.974 Million cell updates/sec

Title: US-09-917-265-52
Perfect score: 921
Sequence: 1 atatgggaactggagaaaga.....gggcatctgtgtcctgcagt 921

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
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6: em_estpl:*
7: em_estro:*
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15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	229	24.9	475	12	BF704417	BF704417 MI-P-E6-a
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c	5	64	6.9	324	17	AQ981401	AQ981401 RPCI-23-3
	6	44.6	4.8	796	13	BI688400	BI688400 603316319
	7	41.6	4.5	540	9	AA004891	AA004891 zh87g02.r
	8	41.4	4.5	595	13	BI983925	BI983925 fu06c08.y
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	11	40.8	4.4	590	10	AW077736	AW077736 fj36h09.y
	12	40.8	4.4	635	13	BI563149	BI563149 fr89b05.y
	13	40.2	4.4	531	13	BM184881	BM184881 ft83f07.y
	14	40	4.3	339	9	AA321223	AA321223 EST23725
	15	39.6	4.3	332	12	BE764332	BE764332 IL5-NT007
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c	17	39.4	4.3	291	10	BB336883	BB336883 BB336883
	18	39.4	4.3	580	9	AA210777	AA210777 zr90d07.r
	19	39.4	4.3	584	10	AW950266	AW950266 EST362336
	20	39.4	4.3	589	14	BM796252	BM796252 K-EST0078
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c	22	39.4	4.3	664	9	AI942458	AI942458 wp80b11.x
	23	39.4	4.3	673	9	AU134439	AU134439 AU134439
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	25	39	4.2	559	10	BE017035	BE017035 fk74f06.y
c	26	38.4	4.2	621	17	AQ199862	AQ199862 RPCI11-46
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c	34	37.6	4.1	660	10	BB626805	BB626805 BB626805
c	35	37.4	4.1	401	9	AL842443	AL842443 AL842443
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ALIGNMENTS

RESULT 1
BF704417
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DEFINITION MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
ACCESSION BF704417
VERSION BF704417.1 GI:11989825
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia,

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            65211 Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .475
                      /organism="Sus scrofa"
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                      /clone_lib="MI-P-E6"
                      /lab_host="DH10B (Life Technologies)"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-E6
                      library is derived from fetus at gestational day 20.  For
                      a detailed description of the  library from which this
                      clone was derived, please visit our web site at
                      http://pigest.genome.iastate.edu/.
                      TAG_SEQ=None found"
BASE COUNT      129 a    120 c    121 g    104 t      1 others
ORIGIN

  Query Match             24.9%;  Score 229;  DB 12;  Length 475;
  Best Local Similarity   78.6%;  Pred. No. 2.6e-50;
  Matches  290;  Conservative    0;  Mismatches   70;  Indels    9;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db        112 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 171

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
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Db        172 GGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCA 231

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        232 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 291

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Db        352 CTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA---------AAAAAT 402

Qy        301 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
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Db        403 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 462

Qy        361 TGGTGGCTG 369
              |  ||| ||
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RESULT 2
AZ441303
LOCUS       AZ441303                 535 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0232M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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ACCESSION   AZ441303
VERSION     AZ441303.1  GI:10565316
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 535.
FEATURES              Location/Qualifiers
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                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0232M24"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT      132 a    135 c    130 g    137 t      1 others
ORIGIN

  Query Match             19.3%;  Score 178.2;  DB 17;  Length 535;
  Best Local Similarity   81.6%;  Pred. No. 1e-36;
  Matches  218;  Conservative    0;  Mismatches   48;  Indels    1;  Gaps    1;

Qy         22 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 81
              |||||||||||||||| ||||||||   || |||||||| |||||||  |||  |||||||
Db         86 GTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCTGGAGAAACAGTGAACCTCACC 145

Qy         82 TGCCATAC-CCCTGAAGAAGATGACATCACTTGGACCTCAGCGCAGAGCAGTGAAGTCCT 140
              ||  | || | |||||||||||||||||||| |||||||||  |||||   || |||| |
Db        146 TGTGACACGCTCTGAAGAAGATGACATCACCTGGACCTCAGACCAGAGACATGGAGTCAT 205

Qy        141 AGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGGAGATGCTGGCCAGTATAC 200
              ||| ||||| || || |||||||||   |||||||| |||  ||||||||||||||| ||
Db        206 AGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTTCTAGATGCTGGCCAGTACAC 265

Qy        201 CTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTGTTGATTCACAAAAAAGAAGA 260
              |||||| |||||||| ||  |||||||| |||||  ||| || | |||||| || ||| |
Db        266 CTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTGCTGCTCCACAAGAAGGAAAA 325

Qy        261 TGGAATTTGGTCCACTGATATCTTAAA 287
              |||||||||||||||||| || |||||
Db        326 TGGAATTTGGTCCACTGAAATTTTAAA 352


RESULT 3
AZ853726/c
```

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LOCUS       AZ853726                569 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157M01 F, DNA sequence.
ACCESSION   AZ853726
VERSION     AZ853726.1  GI:13042136
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: M  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157M01"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      143 a    137 c    153 g    136 t
ORIGIN

  Query Match           18.1%;  Score 166.6;  DB 17;  Length 569;
  Best Local Similarity   80.0%;  Pred. No. 1.3e-33;
  Matches  196;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy         22 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 81
              |||||||||||||| |||||||| || |||||||| ||||||| ||| |||||||
Db        283 GTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCTGGAGAAACAGTGAACCTCACC 224

Qy         82 TGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCAGCGCAGAGCAGTGAAGTCCTA 141
              ||  | || |||||||||||||||||||| |||||||||| ||||| || |||| ||
Db        223 TGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAGAGACATGGAGTCATA 164

Qy        142 GGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGGAGATGCTGGCCAGTATACC 201
              || ||||| || || ||||||||| |||||||| ||| |||||||||||||| |||
Db        163 GGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTTCTAGATGCTGGCCAGTACACC 104

Qy        202 TGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTGTTGATTCACAAAAAAGAAGAT 261
              ||||| ||||||||| ||  |||||||| |||||  ||| || | ||||| || ||| |
Db        103 TGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTGCTGCTCCACAAGAAGGAAAAG 44

Qy        262 GGAAT 266
              | | |
Db         43 GAATT 39


RESULT 4
AG079702/c
LOCUS       AG079702                668 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-075I07.R, genomic survey sequence.
ACCESSION   AG079702
VERSION     AG079702.1  GI:16631504
KEYWORDS    GSS.
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
            BAC Library clone:PTB-075I07.R.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 668)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .668
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PTB-075I07.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      180 a    138 c    137 g    213 t
ORIGIN

  Query Match           10.2%;  Score 93.6;  DB 17;  Length 668;
  Best Local Similarity   79.3%;  Pred. No. 4.4e-14;
  Matches  111;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy        279 TATCTTAAAGGAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAA 338
              | | || |    | |   |||| ||| |  ||| | |||| | | ||| ||| | |||||
Db        561 TTTGTTTATTTCAAATCCAGAACCCAGAGCTAACACCTTTGTAAGATGCGAGACCAAGAA 502

Qy        339 TTATTCTGGACGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAG 398
              |||||| |||||||||||| |||||||||||||| |||||||||||||||||| ||||||
Db        501 TTATTCAGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAG 442

Qy        399 TGTCAAAAGTAGCAGAGGCT 418
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              ||||||||| |||||||| |
Db        441 TGTCAAAAGCAGCAGAGGGT 422


RESULT 5
AQ981401/c
LOCUS       AQ981401                324 bp    DNA     linear   GSS 29-JAN-2000
DEFINITION  RPCI-23-304O12.TJ RPCI-23 Mus musculus genomic clone RPCI-23-304O12
            , DNA sequence.
ACCESSION   AQ981401
VERSION     AQ981401.1  GI:6813702
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-304O12.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 304  row: O  column: 12
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-304O12"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).  "
BASE COUNT      100 a     56 c     60 g    104 t      4 others
ORIGIN

  Query Match             6.9%;  Score 64;  DB 17;  Length 324;
  Best Local Similarity   59.6%;  Pred. No. 2.7e-06;
  Matches  106;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||  || |  ||||  ||  |   |  |  |  | |  | | ||      | |   |||
Db        317 TTTCTTTATTAAAAGAAAACTCCTAAATATTTAATTTTTCTTTTCTTTTCAAATGCAGAT 258

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              | |||||| ||||  || ||||| ||||| |||   ||||| || ||||| ||||| |||
Db        257 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 198

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCT 418
              |  ||||||  |  ||  |  |  || ||||| ||||   || | || || ||  | |
Db        197 TCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCANCATCNAGAGCAGTAGCAGGT 140
```

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RESULT 6
BI688400
LOCUS       BI688400                796 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  6033163191F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5356036 5',
            mRNA sequence.
ACCESSION   BI688400
VERSION     BI688400.1  GI:15651016
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11905  row: f  column: 05
            High quality sequence stop: 779.
FEATURES             Location/Qualifiers
     source          1. .796
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5356036"
                     /clone_lib="NCI_CGAP_Mam6"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      280 a    158 c    175 g    183 t
ORIGIN

  Query Match             4.8%;  Score 44.6;  DB 13;  Length 796;
  Best Local Similarity   48.6%;  Pred. No. 0.57;
  Matches  122;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        189 TGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTGTTGATTCA 248
              ||  ||||  |||||  | |||| |    | | |       |   || || |       |
Db        434 TGTTCAGTCGACCTGATAAAAAGCAACGTATGGTAACTATTGAAAACGCCAGGCACCGAA 493

Qy        249 CAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAAA 308
              | || || ||| | |  ||  |||||  |   | | |||||  |  | |  |   ||||||
Db        494 AACAAGAGCAGAAGCACCTTCATCCACAGCCTTATGAAAGGGAAGGTACAATGGCAAAAA 553

Qy        309 TAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGCT 368
              || | ||   || |     ||  ||  | |    |   |       |    || | |  ||
Db        554 TACGGTCGCGCTAACGGAAGACACACGGCAAATCTTGAGCTAGAACTGGGGCAGTTACCT 613

Qy        369 GACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTCTGACCC 428
                ||    | ||||||||||||  ||| |||    ||  ||  ||  |    |   | |
Db        614 TTCGATCCTAAGTACTGATTTGTGATTAAGTTAGGAAGTTAAGAGCTGTGGATGCTATCT 673

Qy        429 CCAAGGGGTGA 439
              |  ||  |||
Db        674 ACTTGGTTTGA 684


RESULT 7
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AA004891
LOCUS       AA004891                 540 bp    mRNA    linear   EST 07-MAY-1997
DEFINITION  zh87g02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:428306 5', mRNA sequence.
ACCESSION   AA004891
VERSION     AA004891.1  GI:1448568
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1160   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 460.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Homo sapiens"
                     /db_xref="GDB:1328075"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:428306"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.  1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      148 a    103 c    129 g    154 t      6 others
ORIGIN

  Query Match             4.5%;  Score 41.6;  DB 9;  Length 540;
  Best Local Similarity   52.7%;  Pred. No. 3.1;
  Matches   89;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        248 ACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAA 307
              ||  ||  |  || |||| | |   | ||||||  |  | |  |   |||  | |   ||
Db        101 ACTGAACTGTCGAAGGAAATAGCCGCTCTGATAGGTAGATGTGAGTAAAAAGAACAGGAA 160

Qy        308 ATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGC 367
              | ||   |||  |  | ||     |||||||  |  |   ||    ||  |  |||  |
Db        161 AAAATTGCTTCTTTTATTGGTTTCCAAAGAAACAAACCAAACCAACCAGCTCTTGGATGT 220

Qy        368 TGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGG 416
                |   ||  ||| ||  ||||||||  || |  ||||||  |  ||||
Db        221 GAAGATAAAATAGTGCTTTTTTTGAAATGGAGAGGAAAAAGTNGGGGAGG 269
```

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RESULT 8
BI983925
LOCUS       BI983925                 595 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  fu06c08.y3 Campbell zebrafish ovary Danio rerio cDNA clone 5304566
            5' similar to TR:Q9Y3B3 Q9Y3B3 CGI-109 PROTEIN. ;, mRNA sequence.
ACCESSION   BI983925
VERSION     BI983925.1  GI:16374884
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by Library constructed by Invitrogen and
            donated by R. Campbell (Marine Biology Laboratory, Woods Hole, MA).
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 439.
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5304566"
                     /clone_lib="Campbell zebrafish ovary"
                     /sex="female"
                     /dev_stage="4-5 months, 1 year and 2 years"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary(pooled); Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Whole ovaries collected from zebrafish
                     aged 4-5 months, 1 year and 2 years.  Oligo-dT primed,
                     directionally cloned.  Average insert size 2 kb.  Library
                     constructed by Invitrogen and donated by R. Campbell
                     (Marine Biology Laboratory, Woods Hole, MA)."
BASE COUNT      126 a    179 c    161 g    129 t
ORIGIN

  Query Match             4.5%;  Score 41.4;  DB 13;  Length 595;
  Best Local Similarity   52.0%;  Pred. No. 3.7;
  Matches   93;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        467 AGAGGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCA 526
              || |  ||   | ||||| ||         |  |||| |||| | ||||  |||| || ||
Db        267 AGTGTTTCTATGAGGACATCACCATCGGCACCAAGTGCACACTCGAGTTCCAGGTGGTCA 326

Qy        527 GTGCCTGCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACA 586
                |   ||| || || || |||  |||  |      ||   || || |   |   |  |||
Db        327 CCGGGGGCCACTATGACGTGGACTGCCGGCTGGAGGACCCCGAGGGGACGGTGCTCTACA 386

Qy        587 AGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGAC 645
              ||   | | |  |  | |||  ||||  |  ||||| |   |    || |  | |  ||
Db        387 AGGAGATGAAGAAGCAGTACGACAGCTTCACCTTCAGCGCCGCTCGCAACGGAACCTAC 445


RESULT 9
AA002214
LOCUS       AA002214                 490 bp    mRNA    linear   EST 07-MAY-1997
```

```
DEFINITION  zh85a03.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:428044 5', mRNA sequence.
ACCESSION   AA002214
VERSION     AA002214.1  GI:1445109
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1136   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 355.
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Homo sapiens"
                     /db_xref="GDB:1327813"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:428044"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      142 a     94 c    117 g    135 t      2 others
ORIGIN

  Query Match             4.5%;  Score 41;  DB 9;  Length 490;
  Best Local Similarity   52.7%;  Pred. No. 4.4;
  Matches   89;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        248 ACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAA 307
              ||  ||  |  || |||| | |   | ||||||  |  | |  |   |||  | |   ||
Db         86 ACTGAACTGTCGAAGGAAATAGCCGCTCTGATAGGTAGATGTGAGTAAAAAGAACAGGAA 145

Qy        308 ATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGC 367
              | ||   |||  |  | ||     |||||||  |  |   ||    ||  |  |||  |
Db        146 AAAATTGCTTCTTTTATTGGTTTCCAAAGAAACAAACCAAACCAACCAGCTCTTGGATGT 205

Qy        368 TGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGG 416
                |    ||  ||| ||  ||||||||  || |  ||||||  |  ||||
Db        206 GAAGATAAAATAGTGCTTTTTTGAAATGGAGAGGAAAAAGTTGGGGAGG 254


RESULT 10
AI021962/c
LOCUS       AI021962                774 bp    mRNA    linear   EST 28-AUG-1998
DEFINITION  ox05d04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1655431 3' similar to gb:Z29328 UBIQUITIN-CONJUGATING
            ENZYME E2-21 KD (HUMAN);, mRNA sequence.
ACCESSION   AI021962
VERSION     AI021962.1  GI:3237575
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 774)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1053   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 246.
FEATURES             Location/Qualifiers
     source          1. .774
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1655431"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      210 a    179 c    149 g    232 t      4 others
ORIGIN

  Query Match             4.5%;  Score 41;  DB 9;  Length 774;
  Best Local Similarity   52.7%;  Pred. No. 5.1;
  Matches   89;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        248 ACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAA 307
              ||  ||  |  || |||| | |   | ||||||  |  | |  |   |||  | |   ||
Db        256 ACTGAACTGTCGAAGGAAATAGCCGCTCTGATAGGTAGATGTGAGTAAAAAGAACAGGAA 197

Qy        308 ATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGC 367
              | ||   |||  |  | ||     |||||||  |  |   ||    ||  |  |||  |
Db        196 AAAATTGCTTCTTTTATTGGTTTCCAAAGAAACAAACCAAACCAACCAGCTCTTGGATGT 137

Qy        368 TGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGG 416
                |    ||  ||| ||  ||||||||  || |  ||||||  |  ||||
Db        136 GAAGATAAAATAGTGCTTTTTTGAAATGGAGAGGAAAAAGTTGGGGAGG 88


RESULT 11
AW077736
LOCUS       AW077736                590 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fj36h09.y1 zebrafish adult brain Danio rerio cDNA 5' similar to
            WP:F57B10.5 CE11306 ;contains element TAR1 repetitive element ;,
            mRNA sequence.
ACCESSION   AW077736
VERSION     AW077736.1  GI:6032888
KEYWORDS    EST.
SOURCE      zebrafish.
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  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 590)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: T7
            High quality sequence stop: 492.
FEATURES             Location/Qualifiers
     source          1. .590
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone_lib="zebrafish adult brain"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
BASE COUNT      121 a    175 c    171 g    122 t      1 others
ORIGIN

  Query Match             4.4%;  Score 40.8;  DB 10;  Length 590;
  Best Local Similarity   53.8%;  Pred. No. 5.3;
  Matches   84;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        467 AGAGGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCA 526
              || |  ||   | ||||| ||        |  |||| |||| | ||||  |||| || ||
Db        148 AGTGTTTCTATGAGGACATCACCATCGGCACCAAGTGCACACTCGAGTTCCAGGTGGTCA 207

Qy        527 GTGCCTGCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACA 586
              |   ||| || || || ||| |||  |     ||   || || |   |   |  |||
Db        208 CCGGGGGCCACTATGACGTGGACTGCCGGCTGGAGGACCCCGAGGGGACGGTGCTCTACA 267

Qy        587 AGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 622
              ||   | | |  |  | |||  ||||  |  |||||
Db        268 AGGAGATGAAGAAGCAGTACGACAGCTTCACCTTCA 303


RESULT 12
BI563149
LOCUS       BI563149                635 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fr89b05.y1 zebrafish adult brain Danio rerio cDNA clone 4967768 5'
            similar to TR:Q9Y3B3 Q9Y3B3 CGI-109 PROTEIN. ;, mRNA sequence.
ACCESSION   BI563149
VERSION     BI563149.1  GI:15452341
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 635)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: T7
            High quality sequence stop: 369.
FEATURES             Location/Qualifiers
     source          1. .635
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="4967768"
                     /clone_lib="zebrafish adult brain"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
BASE COUNT      125 a    191 c    185 g    134 t
ORIGIN

  Query Match             4.4%;  Score 40.8;  DB 13;  Length 635;
  Best Local Similarity   53.8%;  Pred. No. 5.4;
  Matches   84;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        467 AGAGGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCA 526
              || |  ||   | ||||| ||        |  |||| |||| | ||||  |||| || ||
Db        139 AGTGTTTCTATGAGGACATCACCATCGGCACCAAGTGCACACTCGAGTTCCAGGTGGTCA 198

Qy        527 GTGCCTGCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACA 586
              |   ||| || || || ||| |||  |     ||   || || |   |   |  |||
Db        199 CCGGGGGCCACTATGACGTGGACTGCCGGCTGGAGGACCCCGAGGGGACGGTGCTCTACA 258

Qy        587 AGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 622
              ||   | | |  |  | |||  ||||  |  |||||
Db        259 AGGAGATGAAGAAGCAGTACGACAGCTTCACCTTCA 294


RESULT 13
BM184881
LOCUS       BM184881                531 bp    mRNA    linear   EST 11-DEC-2001
DEFINITION  ft83f07.y3 Gong zebrafish ovary Danio rerio cDNA clone 5159964 5'
            similar to TR:Q9Y3B3 Q9Y3B3 CGI-109 PROTEIN. ;, mRNA sequence.
ACCESSION   BM184881
VERSION     BM184881.1  GI:17515839
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: ft83f07.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            The library was constructed by Dr. Z. Gong. DNA Sequencing by:
            Washington University Genome Sequencing Center St. Louis. Please
            contact Zhiyuan Gong for further information on this library
            (National University of Singapore, Department of Biological
            Sciences, Lower Kent Ridge Road, Singapore 119260).
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 394.
FEATURES             Location/Qualifiers
     source          1. .531
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5159964"
                     /clone_lib="Gong zebrafish ovary"
                     /sex="female"
                     /dev_stage="4-5 month"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary (pooled); Vector: pBluescript SK-;
                     Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
                     the ovaries of 2 female adult zebrafish (4-5 month  old).
                     cDNAs were made using oligo-dT primers and inserted into
                     lambda ZAP II vector  (Stratagene) by Dr. Z. Gong, in vivo
                     mass-excised to pBluescript SK- following the  Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Zhiyuan Gong for further information on
                     this library (National University  of Singapore,
                     Department of Biological Sciences, Lower Kent Ridge Road,
                     Singapore 119260)."
BASE COUNT      110 a    165 c    157 g     99 t
ORIGIN

  Query Match             4.4%;  Score 40.2;  DB 13;  Length 531;
  Best Local Similarity   52.0%;  Pred. No. 7.4;
  Matches   90;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy        473 TCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCT 532
              ||   | ||||| ||        |  |||| |||| | ||||  |||| || ||  |
Db          5 TCTATGAGGACATCACCATCGGCACCAAGTGCACACTCGAGTTCCAGGTGGTCACCGGGG 64

Qy        533 GCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCA 592
              ||| || || || |||  |||  |     ||   || || |   |   |  |||||   |
Db         65 GCCACTATGACGTGGACTGCCGGCTGGAGGACCCCGAGGGGACGGTGCTCTACAAGGAGA 124

Qy        593 AGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGAC 645
               | |  |  | |||  ||||  |  |||||  |   |    || |  | |  ||
Db        125 TGAAGAAGCAGTACGACAGCTTCACCTTCAGCGCCGCTCGCAACGGAACCTAC 177


RESULT 14
AA321223
LOCUS       AA321223                339 bp    mRNA    linear   EST 19-APR-1997
DEFINITION  EST23725 Bone marrow Homo sapiens cDNA 5' end similar to
            ubiquitin-conjugating enzyme UbcH2, 23 kDa, mRNA sequence.
ACCESSION   AA321223
VERSION     AA321223.1  GI:1973591
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
            ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
            ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
            Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
            ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
            Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
            Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.
            , Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
            Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
            Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
            ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
            Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
COMMENT     Other_ESTs: THC174363
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .339
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):121813"
                     /db_xref="taxon:9606"
                     /clone_lib="Bone marrow"
                     /sex="mixed"
                     /tissue_type="bone marrow"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT      101 a     60 c     92 g     84 t      2 others
ORIGIN

  Query Match             4.3%;  Score 40;  DB 9;  Length 339;
  Best Local Similarity   52.1%;  Pred. No. 7.1;
  Matches   88;  Conservative    0;  Mismatches   81;  Indels    0;  Gaps    0;

Qy        248 ACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAA 307
              ||  ||  |  || |||| | |   | ||||||  |  | |  |   |||  | |   ||
Db         45 ACTGAACTGTCGAAGGAAATAGCCGCTCTGATAGGTAGATGTGAGTAAAAAGAACAGGAA 104

Qy        308 ATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGC 367
              | ||   |||  |  | ||     |||||||  |  |   ||    ||  |  |||  |
Db        105 AAAATTGCTTCTTTTATTGGTTTCCAAAGAAACAAACCAAACCAACCAGCTCTTGGATGT 164

Qy        368 TGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGG 416
                |    ||  ||| ||  ||||||||  || |  |||| | |  ||||
Db        165 GAAGATAAAATAGTGCTTTTTTGAAATGGAGAGGAAAAACTNGGGGAGG 213


RESULT 15
BE764332
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LOCUS       BE764332                332 bp    mRNA    linear   EST 19-SEP-2000
DEFINITION  IL5-NT0071-180700-115-g02 NT0071 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE764332
VERSION     BE764332.1  GI:10194256
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 332)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=IL5-NT0071-180
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            Seq primer: puc 18 forward
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                     /dev_stage="Adult"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       92 a     66 c     84 g     90 t
ORIGIN

  Query Match             4.3%;  Score 39.6;  DB 12;  Length 332;
  Best Local Similarity   52.4%;  Pred. No. 9;
  Matches   87;  Conservative    0;  Mismatches   79;  Indels    0;  Gaps    0;

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Search completed: July 16, 2003, 13:00:39
Job time : 1674.03 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 06:24:59 ; Search time 50.7848 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	3	724.2	78.6	987	1	US-08-186-529-1	Sequence 1, Appli
	4	724.2	78.6	987	1	US-08-640-386A-1	Sequence 1, Appli
	5	724.2	78.6	1018	2	US-08-184-009-194	Sequence 194, App
	6	724.2	78.6	1018	2	US-08-458-356-194	Sequence 194, App
	7	724.2	78.6	1018	4	US-08-460-736-194	Sequence 194, App
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	9	724.2	78.6	1560	2	US-08-751-767A-11	Sequence 11, Appl
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	43	32.2	3.5	3107	1	US-07-845-989-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,984A
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 990 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: Canine IL12
; LOCATION: 1 to 987
; IDENTIFICATION METHOD: Similarity
US-09-079-984A-11

Query Match 100.0%; Score 921; DB 4; Length 990;

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RESULT 2
US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

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Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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Db        727 CAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              ||||||||||||| ||||||||
Db        967 TGGGCATCTGTGCCCTGCAGT 987


RESULT 3
US-08-186-529-1
; Sequence 1, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-186-529-1

  Query Match             78.6%;  Score 724.2;  DB 1;  Length 987;
  Best Local Similarity   87.4%;  Pred. No. 9.8e-227;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db         67 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||| | ||||||||||||||||  ||||| |||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||| ||| |||| ||||| ||||| |||||||||||||||||||| |||
Db        187 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||||| ||||| || ||||||||| ||||||| |||  || ||||||
Db        247 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              || |||||||||| |||||||||||||||||||||||| |||||||| |||||||||
Db        307 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||| |||||| | ||| ||||| |||||||||||||||||||||||| |||
Db        367 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||||| |||||||||||||| |||||||||
Db        427 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| || ||||| |  ||||| || |||||||| ||||||| |
Db        487 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||| ||
Db        547 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 603

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| |||||||||  ||||||||||||||||||||
Db        604 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 663

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||||||| |||||||||||||  ||||||||  ||| ||
Db        664 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 723

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||| || |||||||||| |||||||||||||||||| ||||| ||||||
Db        724 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 783

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||||||||| ||| | |||| |||||||||||  |
Db        784 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 843

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        844 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 903

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||  ||||||  ||  ||||||  ||||  ||||||||||||| |||||  ||||||||
Db        904 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 963

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              ||||||||||||  ||||||||
Db        964 TGGGCATCTGTGCCCTGCAGT 984


RESULT 4
US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1

  Query Match             78.6%;  Score 724.2;  DB 1;  Length 987;
  Best Local Similarity   87.4%;  Pred. No. 9.8e-227;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||| ||||||||||||||| ||||| ||||| ||| | || ||||||||
Db         67 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||  | ||||||||||||||||  ||||| |||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||  ||| |||| ||||| ||||| ||||||||||||||||||||| |||
Db        187 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || |||||||| ||||||| |||  || ||||||
Db        247 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              || |||||||||| |||||||||||||||||||||||||||| |||||||| ||||||||
Db        307 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||| |||||| | ||| ||||| |||||||||||||||||||||||| |||
Db        367 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||||| |||||||||||||| ||||||||||
Db        427 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| || ||||| |  ||||| || |||||||| ||||||| |
Db        487 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||  ||
Db        547 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 603

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| |||||||||  ||||||||||||||||||||
Db        604 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 663

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||| |||||||||||| |||||||||  ||| ||
Db        664 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 723

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||||| |||||||||||||||||| ||||| ||||||
Db        724 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 783

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||||||||||| ||| | |||| ||||||||||| |
Db        784 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 843

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||||| ||| |  ||||||||||||||||| |||| | |||| |
Db        844 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 903

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||  ||||||  ||  ||||||  ||||  ||||||||||||| |||||  ||||||||
Db        904 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 963

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              ||||||||||||  ||||||||
Db        964 TGGGCATCTGTGCCCTGCAGT 984


RESULT 5
US-08-184-009-194
; Sequence 194, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
```

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;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-194

  Query Match           78.6%;  Score 724.2;  DB 2;  Length 1018;
  Best Local Similarity  87.4%;  Pred. No. 1e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         98 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 157

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||| | ||||||||||||||| ||||| |||||||
Db        158 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 217

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||| ||| |||| ||||| ||||| |||||||||||||||||||| ||
Db        218 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 277

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || |||||||| ||||||| |||| || ||||||
Db        278 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 337

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
               || |||||||||| ||||||||||||||||||||||||||| |||||||| |||||||||
Db        338 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 397

Qy        301 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||||||| |||
Db        398 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 457

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||||| |||||||||||||| ||||||||||
Db        458 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 517

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| || ||||| |  ||||| || |||||||| ||||||| |
Db        518 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 577

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    |||||  |||||||||| ||||||| ||||||||||  ||
Db        578 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 634

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| ||||||||||  ||||||||||||||||||||
Db        635 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 694

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||| |||||||||||||| ||||||||||  ||| ||

Db        695 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 754

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||||| |||||||||||||||| ||||| ||||||
Db        755 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||||||||||| ||| | |||| ||||||||||| |
Db        815 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 874

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||||| ||| |  ||||||||||||||||| |||| | |||| |
Db        875 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 934

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Db        935 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 994

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        995 TGGGCATCTGTGCCCTGCAGT 1015


RESULT 6
US-08-458-356-194
; Sequence 194, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-194

  Query Match           78.6%;  Score 724.2;  DB 2;  Length 1018;
  Best Local Similarity  87.4%;  Pred. No. 1e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;
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Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db         98 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 157

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||||||
Db        158 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 217

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||| |||
Db        218 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 277

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || ||||||||| ||||||| |||| || ||||||
Db        278 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 337

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
               || |||||||||| |||||||||||||||||||||||||| |||||||| |||||||||
Db        338 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 397

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||| |||
Db        398 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 457

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||||| |||||||||||||| ||||||||||
Db        458 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 517

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| || ||||| |  ||||| || |||||||| ||||||| |
Db        518 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 577

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    ||||| |||||||||| |||||| ||||||||||  ||
Db        578 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 634

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| |||||||||  ||||||||||||||||||||
Db        635 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 694

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||| |||||||||||||| ||||||||||  ||| ||
Db        695 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 754

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||||| |||||||||||||||| ||||| ||||||
Db        755 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||||||||||| ||| | |||| ||||||||||  |
Db        815 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 874

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||| ||| |  |||||||||||||||| |||| | |||| |
Db        875 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 934

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||  |||||| ||  |||||| |||| |||||||||||| ||||| ||||||||
Db        935 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 994

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        995 TGGGCATCTGTGCCCTGCAGT 1015


RESULT 7
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-194

  Query Match             78.6%;  Score 724.2;  DB 4;  Length 1018;
  Best Local Similarity   87.4%;  Pred. No. 1e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db         98 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 157

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||||||
Db        158 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 217

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||| |||
Db        218 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 277

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || |||||||| ||||||| |||| || ||||||
Db        278 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 337

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
               || |||||||||| |||||||||||||||||||||||||| |||||||| |||||||||
Db        338 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 397

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||| |||
Db        398 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 457

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||||| |||||||||||||| ||||||||||
Db        458 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 517

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| || ||||| |  ||||| || |||||||| ||||||| |
Db        518 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 577
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||||  ||
Db        578 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 634

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| |||||||||  |||||||||||||||||||
Db        635 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 694

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||| |||||||||||| ||||||||||  ||| ||
Db        695 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 754

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||||| |||||||||||||||| ||||| ||||||
Db        755 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||||||||| ||| | |||| ||||||||||| |
Db        815 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 874

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||| ||| |  |||||||||||||||| |||| | |||| |
Db        875 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 934

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||  ||||||  ||  ||||||  |||| ||||||||||||| ||||| ||||||||
Db        935 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 994

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        995 TGGGCATCTGTGCCCTGCAGT 1015


RESULT 8
US-08-751-767A-3
; Sequence 3, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..1026
US-08-751-767A-3

  Query Match            78.6%;  Score 724.2;  DB 2;  Length 1399;
  Best Local Similarity  87.4%;  Pred. No. 1.2e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db        109 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 168

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||||||
Db        169 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 228

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||| ||| |||| ||||| ||||| |||||||||||||||||||||| |||
Db        229 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 288

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || |||||||| ||||||| |||| || ||||||
Db        289 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 348

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              || |||||||||| ||||||||||||||||||||||||||| |||||||| ||||||||
Db        349 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 408

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||| |||||| | ||| |||| ||||||||||||||||||||||||| |||
Db        409 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 468

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||| |||||||||||||| ||||||||||
Db        469 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 528

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||| || ||||| |  ||||| || |||||||| ||||||| |
Db        529 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 588

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    ||||| |||||||||| |||||| ||||||||||||  ||
Db        589 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 645

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| |||||||||  |||||||||||||||||||
Db        646 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 705

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||| |||||||||||| ||||||||||  ||| ||
Db        706 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 765

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||||| |||||||||||||||| ||||| ||||||
Db        766 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 825

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||||||||| ||| | |||| |||||||||| |
Db        826 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 885

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||| ||| |  ||||||||||||||||| |||| | |||| |
Db        886 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 945

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||  ||||||  ||  ||||||  |||| ||||||||||||| ||||| ||||||||
Db        946 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 1005

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db       1006 TGGGCATCTGTGCCCTGCAGT 1026
```

```
RESULT 9
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1557
US-08-751-767A-11

  Query Match           78.6%;  Score 724.2;  DB 2;  Length 1560;
  Best Local Similarity  87.4%;  Pred. No. 1.3e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db          4 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 63

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||  | ||||||||||||||||  ||||| |||||||
Db         64 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 123

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||| |||
Db        124 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 183

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || |||||||| ||||||| ||||  || ||||||
Db        184 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 243

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              || |||||||||| |||||||||||||||||||||||| |||||||| |||||||||
Db        244 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 303

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||| |||||| | ||| ||||| |||||||||||||||||||||| |||

Db        304 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 363

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||| |||||||||||||| ||||||||||
Db        364 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 423

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||||||
Db        424 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 483

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||||  ||
Db        484 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| |||||||||| ||||||||||||||||||||
Db        541 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||||| |||||||||||||| |||||||||  ||| ||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 660

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||||| |||||||||||||||| ||||| ||||||
Db        661 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||||||||||| ||| | |||| ||||||||| |
Db        721 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 780

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||||| ||| | |||||||||||||||| |||| | |||| |
Db        781 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||  ||||||  ||  ||||||  ||||  |||||||||||||| ||||| ||||||||
Db        841 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 900

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        901 TGGGCATCTGTGCCCTGCAGT 921


RESULT 10
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

  Query Match             78.6%;  Score 724.2;  DB 2;  Length 1623;
  Best Local Similarity   87.4%;  Pred. No. 1.3e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db         67 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||| ||| |||| ||||| ||||| |||||||||||||||||||| |||
Db        187 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || ||||||||| ||||||| |||| || ||||||
Db        247 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              || |||||||||| |||||||||||||||||||||||||| |||||||| |||||||||
Db        307 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||| |||
Db        367 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||||| |||||||||||||| ||||||||||
Db        427 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| || ||||| |  ||||| || |||||||| ||||||| |
Db        487 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||||  ||
Db        547 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 603

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| |||||||||| ||||||||||||||||||||
Db        604 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 663

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||||| |||||||||||||| |||||||||  ||| ||
Db        664 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 723

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||||| ||||||||||||||| ||||| ||||||
Db        724 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 783

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||||||||||| ||| | |||| |||||||||| |
Db        784 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 843

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || ||||||||||||||||| ||| |  |||||||||||||||| |||| | |||| |

Db        844 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 903

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||  ||||||  ||  ||||||  |||| ||||||||||||| ||||| ||||||||
Db        904 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 963

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        964 TGGGCATCTGTGCCCTGCAGT 984


RESULT 11
US-08-265-087-1
; Sequence 1, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-265-087-1

  Query Match             78.6%;  Score 724.2;  DB 1;  Length 2362;
  Best Local Similarity   87.4%;  Pred. No. 1.7e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db         99 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 158

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||||||
Db        159 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 218

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||| ||| |||| ||||| ||||| |||||||||||||||||||| |||
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Db        219 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 278

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Db        279 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 338

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Db        339 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 398

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Db        399 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 458

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Db        459 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 518

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Db        519 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 578

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Db        579 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 635

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Db        636 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 695

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Db        696 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 755

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Db        756 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 815

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Db        816 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 875

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        876 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 935

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Db        936 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 995

Qy        901 TGGGCATCTGTGTCCTGCAGT 921

Db        996 TGGGCATCTGTGCCCTGCAGT 1016


RESULT 12
US-08-621-493-1
; Sequence 1, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-621-493-1

  Query Match             78.6%;  Score 724.2;  DB 1;  Length 2362;
  Best Local Similarity   87.4%;  Pred. No. 1.7e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Db         99 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 158

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Db        159 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 218

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Db        219 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 278

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Db        279 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 338

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Db        339 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 398

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Db        399 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 458

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Db        459 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 518

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Db        519 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 578

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Db        579 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 635

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        636 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 695

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
                 |||||||||||||||||||||||||| |||||||||||||| |||||||||  ||| ||
Db        696 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 755

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
                 |||||||||||||| || |||||||||| |||||||||||||||| ||||| ||||||
Db        756 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 815

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
                 ||||| || ||||||||||||||||||||||||| ||| | |||| |||||||||| |
Db        816 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 875

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                 || |||||||||||||||| ||| | |||||||||||||||| |||| | |||| |
Db        876 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 935

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
                 ||  ||||||  ||  ||||||  |||| ||||||||||||| ||||| ||||||||
Db        936 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 995

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db        996 TGGGCATCTGTGCCCTGCAGT 1016


RESULT 13
US-08-965-688-1
; Sequence 1, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-965-688-1

  Query Match             78.6%;  Score 724.2;  DB 2;  Length 2362;
  Best Local Similarity   87.4%;  Pred. No. 1.7e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db         99 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 158

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||| | ||||||||||||||| ||||| |||||||
Db        159 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 218

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||||| ||| |||| ||||| ||||| ||||||||||||||||||||| |||
Db        219 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 278

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || |||||||| ||||||| |||| || ||||||
Db        279 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 338

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              || |||||||||| ||||||||||||||||||||||||| |||||||| |||||||||
Db        339 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 398

Qy        301 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||| |||||| | ||| ||||| |||||||||||||||||||||||| |||
Db        399 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 458

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||| |||||||||||||||| |||||||||||||| ||||||||||
Db        459 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 518

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Db        519 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 578

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||||  ||
Db        579 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 635

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              || |||||||| || ||||| |||||| ||||||||||  ||||||||||||||||||||
Db        636 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 695

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||| |||||||||||||| |||||||||  ||| ||
Db        696 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 755

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              |||||||||||||| || |||||||||| |||||||||||||||| ||||| ||||||
Db        756 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 815

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||| || ||||||||||||||||||||||||| ||| | |||| |||||||||| |
Db        816 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 875

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||| ||| | |||||||||||||||| |||| | |||| |
Db        876 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 935

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||  ||||||  ||  ||||||  |||| ||||||||||||| ||||| ||||||||
Db        936 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 995

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||| ||||||||
Db        996 TGGGCATCTGTGCCCTGCAGT 1016
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Db        996 TGGGCATCTGTGCCCTGCAGT 1016


RESULT 14
US-09-260-173-1
; Sequence 1, Application US/09260173
; Patent No. 6168923
;  GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2362 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  33..1016
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

  Query Match             78.6%;  Score 724.2;  DB 4;  Length 2362;
  Best Local Similarity   87.4%;  Pred. No. 1.7e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||||
Db         99 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 158

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||||||
Db        159 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 218

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||| |||
Db        219 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 278

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              |||||||||||||||| ||||| || |||||||| ||||||| |||| || ||||||
Db        279 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 338

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
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Db        339 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 398

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Db        519 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 578

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Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        636 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 695

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
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RESULT 15
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             78.6%;  Score 724.2;  DB 2;  Length 6139;
  Best Local Similarity   87.4%;  Pred. No. 3.1e-226;
  Matches  805;  Conservative    0;  Mismatches  113;  Indels    3;  Gaps    1;

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Job time : 53.7848 secs
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:38:23 ; Search time 180.229 Seconds
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8158.492 Million cell updates/sec

Title: US-09-917-265-52
Perfect score: 921
Sequence: 1 atatgggaactggagaaaga.....gggcatctgtgtcctgcagt 921

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1114047 seqs, 798260406 residues

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		921	100.0	921	10	US-09-917-265-52	Sequence 52, Appl
2	c	921	100.0	921	10	US-09-917-265-54	Sequence 54, Appl
3		921	100.0	2267	10	US-09-917-265-107	Sequence 107, App
4	c	921	100.0	2267	10	US-09-917-265-109	Sequence 109, App
5		919.4	99.8	987	10	US-09-917-265-58	Sequence 58, Appl
6	c	919.4	99.8	987	10	US-09-917-265-60	Sequence 60, Appl
7		919.4	99.8	1533	10	US-09-917-265-66	Sequence 66, Appl
8	c	919.4	99.8	1533	10	US-09-917-265-68	Sequence 68, Appl
9		919.4	99.8	1599	10	US-09-917-265-61	Sequence 61, Appl
10	c	919.4	99.8	1599	10	US-09-917-265-63	Sequence 63, Appl
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12		826.6	89.8	987	10	US-09-917-265-29	Sequence 29, Appl
13	c	826.6	89.8	987	10	US-09-917-265-31	Sequence 31, Appl
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15		825	89.6	921	10	US-09-917-265-26	Sequence 26, Appl
16	c	825	89.6	921	10	US-09-917-265-28	Sequence 28, Appl
17		825	89.6	921	12	US-10-079-616-7	Sequence 7, Appli
18		825	89.6	1533	10	US-09-917-265-43	Sequence 43, Appl
19	c	825	89.6	1533	10	US-09-917-265-45	Sequence 45, Appl
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21	c	825	89.6	1599	10	US-09-917-265-40	Sequence 40, Appl
22		824.6	89.5	985	10	US-09-917-265-55	Sequence 55, Appl
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26		724.2	78.6	2362	10	US-09-924-703-3	Sequence 3, Appli
27		722.6	78.5	987	9	US-09-826-025-24	Sequence 24, Appl
28		722.6	78.5	1870	9	US-10-228-811-4	Sequence 4, Appli
29		722.6	78.5	2318	9	US-10-172-399-7	Sequence 7, Appli
30		722.6	78.5	8578	10	US-09-828-825-1	Sequence 1, Appli
31		722.6	78.5	8578	10	US-09-828-825-3	Sequence 3, Appli
32		722.6	78.5	8608	10	US-09-828-825-7	Sequence 7, Appli
33		722.6	78.5	8623	10	US-09-828-825-5	Sequence 5, Appli
34		722.6	78.5	8629	10	US-09-828-825-15	Sequence 15, Appl
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36		722.6	78.5	8644	10	US-09-828-825-13	Sequence 13, Appl
37		722.6	78.5	8659	10	US-09-828-825-11	Sequence 11, Appl
38		562.8	61.1	987	10	US-09-754-014-4	Sequence 4, Appli
39		531.2	57.7	987	10	US-09-754-014-3	Sequence 3, Appli
40		466	50.6	1840	9	US-10-172-399-3	Sequence 3, Appli
41		39.4	4.3	594	9	US-10-123-155-10	Sequence 10, Appl
42		39.4	4.3	594	9	US-10-146-731-10	Sequence 10, Appl
43	c	39.4	4.3	625	10	US-09-879-536-593	Sequence 593, App
44		39.4	4.3	2005	9	US-10-171-581-281	Sequence 281, App
45		39.4	4.3	2723	9	US-10-098-841-216	Sequence 216, App

ALIGNMENTS

RESULT 1
US-09-917-265-52
; Sequence 52, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION:
US-09-917-265-52

Query Match 100.0%; Score 921; DB 10; Length 921;
Best Local Similarity 100.0%; Pred. No. 3.9e-289;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        901 TGGGCATCTGTGTCCTGCAGT 921


RESULT 2
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-54
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  Query Match           100.0%;  Score 921;  DB 10;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-289;
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Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 682

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 502

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 382

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 262

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 142

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 22

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCTGTGTCCTGCAGT 1


RESULT 3
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
;   OTHER INFORMATION:
US-09-917-265-107

  Query Match             100.0%;  Score 921;  DB 10;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-289;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 279

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 339

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 399

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 459

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 519

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 579

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 639

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 699

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 759

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 879

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 939

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 999

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 1059

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 1119

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1120 TGGGCATCTGTGTCCTGCAGT 1140


RESULT 4
US-09-917-265-109/c
; Sequence 109, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-109

  Query Match             100.0%;  Score 921;  DB 10;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-289;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2048 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1989

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1988 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1929

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1928 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1869

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1868 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1809

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1808 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1749

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1748 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1689

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1688 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1629

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1628 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1569
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 1509

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 1389

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 1329

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 1269

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 1209

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 1149

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1148 TGGGCATCTGTGTCCTGCAGT 1128
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RESULT 5
US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-58

  Query Match            99.8%;  Score 919.4;  DB 10;  Length 987;
  Best Local Similarity  99.9%;  Pred. No. 1.3e-288;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||||||||||| ||||||
Db        967 TGGGCATCTGTGTCATGCAGT 987
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```
RESULT 6
US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
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;   ORGANISM: Canis familiaris
US-09-917-265-60

  Query Match            99.8%;  Score 919.4;  DB 10;  Length 987;
  Best Local Similarity  99.9%;  Pred. No. 1.3e-288;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 802

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 682

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 502

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 382

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 262

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 142

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 22

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              ||||||||||||||| ||||||
Db         21 TGGGCATCTGTGTCATGCAGT 1

RESULT 7
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match            99.8%;  Score 919.4;  DB 10;  Length 1533;
  Best Local Similarity  99.9%;  Pred. No. 1.8e-288;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
                |||||||||||||| ||||||
Db        901 TGGGCATCTGTGTCATGCAGT 921


RESULT 8
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             99.8%;  Score 919.4;  DB 10;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 1.8e-288;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
                |||||||||||||| ||||||
Db        633 TGGGCATCTGTGTCATGCAGT 613


RESULT 9
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             99.8%;  Score 919.4;  DB 10;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 1.8e-288;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
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Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              ||||||||||||||| ||||||
Db        967 TGGGCATCTGTGTCATGCAGT 987
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RESULT 10
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match            99.8%;  Score 919.4;  DB 10;  Length 1599;
  Best Local Similarity  99.9%;  Pred. No. 1.8e-288;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              ||||||||||||||| ||||||
Db        633 TGGGCATCTGTGTCATGCAGT 613
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```
RESULT 11
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match             89.8%;  Score 826.6;  DB 12;  Length 921;
  Best Local Similarity   93.6%;  Pred. No. 2.1e-258;
  Matches  862;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||| |||| ||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              | |||||||||||||||||||| |||||||||||| ||||||||||||  ||  ||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||  |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||||| |||||||||||| |||||||| |||||||||  |
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||||| |||||||||| |||||| |||||||||| ||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              |||||||||||||||||||| || |||||||||| ||||||||||||||||||||| |||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||| |||||||||||| |||||||||  ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || |||||||||| |||||||||||| ||||| || ||||||||||||| ||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||| ||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||| ||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 12
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
```

US-09-917-265-29

Query Match 89.8%; Score 826.6; DB 10; Length 987;
Best Local Similarity 93.6%; Pred. No. 2.2e-258;
Matches 862; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||| |||| |||||||||||||||||||| ||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
               |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||| |||||||||| ||||| |||||||||| ||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              |||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||| |||||||||||| |||||||||  ||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || |||||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| |||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||| ||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987
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RESULT 13
US-09-917-265-31/c

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; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31
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Query Match 89.8%; Score 826.6; DB 10; Length 987;
Best Local Similarity 93.6%; Pred. No. 2.2e-258;
Matches 862; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

```
Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||| |||| |||||||||||||||||||| ||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
               |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
              |||||||||||||||||| |||||||||| ||||| |||||||||| ||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
              |||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||| |||||||||||| |||||||||  ||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || |||||||||||| |||||||||||||| |||||| || |||||||||||||| ||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
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Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || ||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
              |||||||| ||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 14
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             89.8%;  Score 826.6;  DB 12;  Length 2193;
  Best Local Similarity   93.6%;  Pred. No. 3.7e-258;
  Matches  862;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||

Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
              |||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              |||| |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540
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Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
              |||||||||||||||||||||||||| |||||||||||||| |||||||||  ||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
              || |||||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 15
US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
```

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;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-26
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Query Match 89.6%; Score 825; DB 10; Length 921;
Best Local Similarity 93.5%; Pred. No. 7.1e-258;
Matches 861; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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Qy         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240
              | ||||||||||||||||||||| |||||||||||  ||||||||||||  ||  ||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300
              ||||  |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
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Qy        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
              |||||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660
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Qy        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
              |||||||||||||||||||||||||||| ||||||||||||||| |||||||||||| ||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCTGTGTCCTGCAGT 921
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Search completed: July 16, 2003, 13:16:27
Job time : 182.229 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:54:38 ; Search time 30.8609 Seconds
(without alignments)
1325.559 Million cell updates/sec

Title: US-09-917-265-53
Perfect score: 1653
Sequence: 1 IWELEKDVYVVELDWHPDAP.....QARDRYYSSSWSDWASVSCS 307

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1653	100.0	329	19	AAW41791	Canine IL-12 P40 s
2	1653	100.0	329	20	AAY02342	Canine Interleukin
3	1653	100.0	329	20	AAW84373	Canine interleukin
4	1653	100.0	329	22	AAG66482	Canine protein #3.
5	1644	99.5	329	19	AAW41790	Canine IL-12 P40 s
6	1644	99.5	329	20	AAY02339	Canine Interleukin
7	1644	99.5	329	20	AAW84371	Canine interleukin
8	1644	99.5	329	22	AAG66480	Canine protein #1.
9	1618.5	97.9	308	20	AAW74323	Canine mature CLAF
10	1618.5	97.9	330	20	AAW74322	Canine full length
11	1554	94.0	307	19	AAW76174	Feline FLAFp40 mat
12	1554	94.0	329	19	AAW76173	Feline FLAFp40 pro
13	1484	89.8	329	22	AAE08602	Modified human cyt
14	1451	87.8	327	22	AAE08599	Modified human cyt
15	1429	86.4	327	22	AAE08598	Modified human cyt
16	1421	86.0	327	22	AAE08597	Modified human cyt
17	1419.5	85.9	328	23	AAU75579	Human interleukin
18	1419.5	85.9	526	23	AAE19818	Human IL-12.0 prot
19	1419.5	85.9	527	23	AAE19817	Human IL-12.1 prot
20	1419.5	85.9	537	23	AAE19820	Human IL-12.2 prot
21	1419.5	85.9	542	23	AAE19819	Human IL-12.3 prot
22	1419.5	85.9	547	23	AAE19821	Human IL-12.4 prot
23	1418.5	85.8	306	16	AAR63018	IL-12 p40 subunit.
24	1418.5	85.8	306	19	AAW71244	Human IL-12p40. H
25	1418.5	85.8	306	19	AAW58707	Cytotoxic lymphocy
26	1418.5	85.8	328	13	AAR22769	Natural killer cel
27	1418.5	85.8	328	16	AAR79186	Human interleukin-
28	1418.5	85.8	328	17	AAW07398	Human interleukin-
29	1418.5	85.8	328	18	AAW24235	40 kDa subunit of
30	1418.5	85.8	328	18	AAW36941	40 kDa subunit of
31	1418.5	85.8	328	18	AAW36939	40 kDa subunit of
32	1418.5	85.8	328	19	AAW62992	Human interleukin-
33	1418.5	85.8	328	19	AAW58725	Cytotoxic lymphocy
34	1418.5	85.8	328	19	AAW51311	Human Interleukin-
35	1418.5	85.8	328	19	AAW57482	Human interleukin-
36	1418.5	85.8	328	19	AAW51221	Human interleukin-
37	1418.5	85.8	328	19	AAW44324	Heterodimeric huma
38	1418.5	85.8	328	20	AAY42487	Human interleukin
39	1418.5	85.8	328	21	AAB23796	Human interleukin
40	1418.5	85.8	328	21	AAY54919	Human p40 protein
41	1418.5	85.8	328	21	AAY44181	Human interleukin-
42	1418.5	85.8	328	22	AAE11198	Human interleukin-
43	1418.5	85.8	328	22	AAE08603	Human cytokine p40
44	1418.5	85.8	328	22	AAB67262	IL-12 vaccine adju
45	1418.5	85.8	328	22	AAB36649	Human cytokine rec

ALIGNMENTS

RESULT 1
AAW41791
ID AAW41791 standard; peptide; 329 AA.
XX
AC AAW41791;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit.
XX
KW Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant.
XX
OS Canis sp.
XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.
DR N-PSDB; AAV13817.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT activities are expected
XX

PS Claim 2; Pages 10-11; 12pp; Japanese.
XX
CC The present sequence is a canine interleukin-12 (IL-12) P40
CC subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antivirus and
CC vaccine adjuvant activities are expected.
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1653; DB 19; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
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Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
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Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
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Db        323 WASVSCS 329
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RESULT 2
AAY02342
ID AAY02342 standard; Protein; 329 AA.
XX
AC AAY02342;
XX
DT 09-JUL-1999 (first entry)
XX
DE Canine Interleukin-12 (IL-12) protein sequence.
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease.
XX
OS Canis sp.
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR N-PSDB; AAX35625.
XX
PT A prevention and treating agent containing interleukin 12 (CaIL12) -
PT for prevention and treatment of dog and cat immune diseases
XX
PS Claim 1; Page 14-15; 16pp; Japanese.
XX
CC The present sequence represents canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1653; DB 20; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
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Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329
```

RESULT 3
AAW84373
ID AAW84373 standard; Protein; 329 AA.
XX
AC AAW84373;
XX
DT 30-MAR-1999 (first entry)
XX
DE Canine interleukin 12 protein.
XX
KW Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;
KW oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW feline leukaemia; allergy; pollinosis.
XX
OS Canis sp.
XX
PN WO9851327-A1.
XX
PD 19-NOV-1998.
XX
PF 07-MAY-1998; 98WO-JP02031.
XX
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX

```
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03162.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   329 AA;

  Query Match             100.0%;  Score 1653;  DB 20;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-139;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 4
AAG66482
ID   AAG66482 standard; Protein; 329 AA.
XX
AC   AAG66482;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         23..329
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64388.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   329 AA;

  Query Match             100.0%;  Score 1653;  DB 22;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-139;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 5
AAW41790
ID   AAW41790 standard; peptide; 329 AA.
XX
AC   AAW41790;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant.
XX
OS   Canis sp.
```

XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.
DR N-PSDB; AAV13816.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT activities are expected
XX
PS Claim 2; Page 8; 12pp; Japanese.
XX
CC The present sequence is a canine interleukin-12 (IL-12) P40
CC subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antivirus and
CC vaccine adjuvant activities are expected.
XX
SQ Sequence 329 AA;

Query Match 99.5%; Score 1644; DB 19; Length 329;
Best Local Similarity 99.3%; Pred. No. 6.9e-139;
Matches 305; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLENSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||| ||
Db        323 WASVPCS 329
```

RESULT 6
AAY02339
ID AAY02339 standard; Protein; 329 AA.
XX
AC AAY02339;
XX
DT 09-JUL-1999 (first entry)
XX
DE Canine Interleukin-12 (IL-12) protein sequence.
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease.

XX
OS Canis sp.
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR N-PSDB; AAX35615.
XX
PT A prevention and treating agent containing interleukin 12 (CaIL12) -
PT for prevention and treatment of dog and cat immune diseases
XX
PS Claim 1; Page 12; 16pp; Japanese.
XX
CC The present sequence represents canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
SQ Sequence 329 AA;

Query Match 99.5%; Score 1644; DB 20; Length 329;
Best Local Similarity 99.3%; Pred. No. 6.9e-139;
Matches 305; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLENSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||| ||
Db        323 WASVPCS 329
```

RESULT 7
AAW84371
ID AAW84371 standard; Protein; 329 AA.
XX
AC AAW84371;
XX
DT 30-MAR-1999 (first entry)
XX
DE Canine interleukin 12 protein.
XX
KW Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;

```
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03152.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   329 AA;

  Query Match             99.5%;  Score 1644;  DB 20;  Length 329;
  Best Local Similarity   99.3%;  Pred. No. 6.9e-139;
  Matches  305;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLENSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              ||||  ||
Db        323 WASVPCS 329
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RESULT 8
AAG66480
ID   AAG66480 standard; Protein; 329 AA.
XX
AC   AAG66480;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         23..329
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64378.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   329 AA;

  Query Match             99.5%;  Score 1644;  DB 22;  Length 329;
  Best Local Similarity   99.3%;  Pred. No. 6.9e-139;
  Matches  305;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLENSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
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Qy        301 WASVSCS 307
              |||| ||
Db        323 WASVPCS 329


RESULT 9
AAW74323
ID   AAW74323 standard; Protein; 308 AA.
XX
AC   AAW74323;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p40 subunit.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   N-PSDB; AAX18177.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 1; Page 24-26; 51pp; Japanese.
XX
CC   This sequence is the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence   308 AA;

  Query Match            97.9%;  Score 1618.5;  DB 20;  Length 308;
  Best Local Similarity  98.4%;  Pred. No. 1.2e-136;
  Matches  303;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLL-IHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 119
              |||||||||||||||||||    ||:|||||||||||||||||||||||||||||||||||
Db         61 GDAGQYTCHKGGKVLSRSLLFDSTKKKDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 120

Qy        120 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 180

Qy        180 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 240

Qy        240 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 300

Qy        300 DWASVSCS 307
              ||||||||
Db        301 DWASVSCS 308


RESULT 10
AAW74322
ID   AAW74322 standard; Protein; 330 AA.
XX
AC   AAW74322;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   N-PSDB; AAX18176.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 1; Page 22-24; 51pp; Japanese.
XX
CC   This sequence is the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence   330 AA;

  Query Match            97.9%;  Score 1618.5;  DB 20;  Length 330;
  Best Local Similarity  98.4%;  Pred. No. 1.3e-136;
  Matches  303;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLL-IHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 119
              |||||||||||||||||||    ||:|||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLFDSTKKKDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 142

Qy        120 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        143 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 202

Qy        180 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 262

Qy        240 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 322

Qy        300 DWASVSCS 307
              ||||||||
Db        323 DWASVSCS 330


RESULT 11
AAW76174
ID   AAW76174 standard; Protein; 307 AA.
XX
AC   AAW76174;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 mature protein.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   N-PSDB; AAV56626, AAV56627.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 3; Page 47-49; 94pp; Japanese.
XX
CC   This sequence represents a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment
CC   of feline autoimmune diseases e.g. as caused by feline herpes virus
CC   or feline calcivirus.
XX
SQ   Sequence   307 AA;

  Query Match            94.0%;  Score 1554;  DB 19;  Length 307;
  Best Local Similarity   93.8%;  Pred. No. 7.3e-131;
  Matches  288;  Conservative    9;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||||||||||||:|||||||||| ||||||||||||||||||
Db          1 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||||:||| | ||||||||||||||:||||||||||||||||||||||
Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||:|||||| |||||||||| |||||:|||||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        301 WASVSCS 307
              |||||||
Db        301 WASVSCS 307


RESULT 12
AAW76173
ID   AAW76173 standard; Protein; 329 AA.
XX
AC   AAW76173;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 protein.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= signal
FT   Protein         23..329
FT                   /label= FLAFp40
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   N-PSDB; AAV56625.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 1; Page 45-47; 94pp; Japanese.
XX
CC   This sequence represents a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence   329 AA;

  Query Match            94.0%;  Score 1554;  DB 19;  Length 329;
  Best Local Similarity   93.8%;  Pred. No. 8e-131;
  Matches  288;  Conservative    9;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||||||||||||:|||||||||| ||||||||||||||||||
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Db         23 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| | ||||||||||||||||:||||||||||||||||||||||
Db         83 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||:|||||| |||||||||| |||||:|||||||||||||||||||||:
Db        143 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||:
Db        263 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 13
AAE08602
ID   AAE08602 standard; Protein; 329 AA.
XX
AC   AAE08602;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 from clone R16-51.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p40; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   1..22
FT                   /label= Leader_peptide
FT   Protein         23..329
FT                   /note= "Mature modified p40"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   N-PSDB; AAD15209.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 38; Fig 1; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein.
XX
SQ   Sequence   329 AA;

  Query Match             89.8%;  Score 1484;  DB 22;  Length 329;
  Best Local Similarity   89.6%;  Pred. No. 1.5e-124;
  Matches  275;  Conservative   13;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||:|||||||||| | ||||| ||||| |||||||:|||||| ||||
Db         23 IWELEKNVYVVELDWYPDAPGEMVVLACDTPEEDGITWTSDQSSEVLGTGKTLTIHVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||| ||| |||:||||:|||||||||||||:||| ||||||||||||||||||
Db         83 GDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQKEPKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||:|||||| |||||||||||||||| :|:|:|: ||||||||||||||
Db        143 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAVTLSAERVSMDHREYNKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||||| |||||||||||||:|||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEISWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              || ||||||| | :| |||| ||||||| ||||||||||||||||||||||||||||:
Db        263 WSIPHSYFSLMFGVQVQGKNKREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSE 322

Qy        301 WASVSCS 307
              |||| ||
Db        323 WASVPCS 329


RESULT 14
AAE08599
ID   AAE08599 standard; Protein; 327 AA.
XX
AC   AAE08599;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 from clone B1-81.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p40; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   1..22
FT                   /label= Leader_peptide
FT   Protein         23..327
FT                   /note= "Mature modified p40"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
```

```
DR   N-PSDB; AAD15206.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 38; Fig 1; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein.
XX
SQ   Sequence   327 AA;

  Query Match             87.8%;  Score 1451;  DB 22;  Length 327;
  Best Local Similarity   87.3%;  Pred. No. 1.4e-121;
  Matches  268;  Conservative   18;  Mismatches   19;  Indels    2;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||||:|||||| ||| | ||||| ||||| |||||||:|||||| ||||
Db         23 IWELEKNVYVVELDWYPDAPGETVVLACDTPEEDGITWTSDQSSEVLGTGKTLTIHVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||| ||| |||:||||:||||||||||||||:||: ||||||||||||||||||
Db         83 GDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQKKPKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||:|||||| |||||||||||||||||| :|:|:| ||||||||||||||
Db        143 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAVTLSAERVSMDHREYNKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||| |||||||||||| |||||:|||||||||:|||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSRFFIRDIIKPDPPKNLQLRPLKNSRHVEISWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||:| |||| |||| | :|:||||| ||||||||||||||:|||||:
Db        263 WSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVTCHKDAKIRVQARDRYHSSSWSE 320

Qy        301 WASVSCS 307
              |||| ||
Db        321 WASVPCS 327


RESULT 15
AAE08598
ID   AAE08598 standard; Protein; 327 AA.
XX
AC   AAE08598;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 from clone B2-52.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p40; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   1..22
FT                   /label= Leader_peptide
FT   Protein         23..327
FT                   /note= "Mature modified p40"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   N-PSDB; AAD15205.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 38; Fig 1; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein.
XX
SQ   Sequence   327 AA;

  Query Match             86.4%;  Score 1429;  DB 22;  Length 327;
  Best Local Similarity   86.6%;  Pred. No. 1.3e-119;
  Matches  266;  Conservative   16;  Mismatches   23;  Indels    2;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||||:|||||||| | ||||| ||||| ||| |||:|||||| ||||
Db         23 IWELEKNVYVVELDWYPDAPGEMVVLACDTPEEDGITWTSDQSSGVLGTGKTLTIHVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||| ||| |||:||||:||||||||||||||:||| | | |||||||:||| |||
Db         83 GDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| |||||||||||||| |||||||||||||||||| :|:|:| ||||||||||||||
Db        143 WWLTTISTDLKFSVKSSRGSSDPQGVTCGAVTLSAERVSMDHREYNKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||||||||| ||||:|||||| |||:||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVNWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||:| |||| |||| | :|:||||| ||||||||||||||||||||||:
Db        263 WSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVTCHKDAKIRVQARDRYYSSSWSE 320

Qy        301 WASVSCS 307
              |||| ||
Db        321 WASVPCS 327


Search completed: July 15, 2003, 11:02:52
Job time : 31.8609 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:49 ; Search time 13.4559 Seconds
(without alignments)
2193.328 Million cell updates/sec

Title: US-09-917-265-53
Perfect score: 1653
Sequence: 1 IWELEKDVYVVELDWHPDAP.....QARDRYYSSSWSDWASVSCS 307

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1418.5	85.8	328	2	A38957	interleukin 12B pr
2	1058.5	64.0	335	2	I72789	interleukin 12 p40
3	193	11.7	468	1	A41242	interleukin-6 rece
4	178	10.8	362	2	S60614	growth promoting a
5	176.5	10.7	440	2	JL0144	interleukin-6 rece
6	176.5	10.7	460	2	JL0145	interleukin-6 rece
7	173	10.5	372	2	I58141	ciliary neurotroph
8	170	10.3	372	1	UHHUCN	ciliary neurotroph
9	149.5	9.0	422	2	I37891	interleukin-11 rec
10	146.5	8.9	432	2	I48343	interleukin-11 rec
11	132	8.0	812	2	H96544	hypothetical prote
12	122.5	7.4	1277	2	T30532	neural cell adhesi
13	114	6.9	831	2	JQ1655	prolactin receptor
14	114	6.9	977	2	I45877	protein-tyrosine k
15	111.5	6.7	310	2	A29884	prolactin receptor
16	111.5	6.7	412	2	A41070	prolactin receptor
17	111.5	6.7	610	2	A34631	lactogen receptor
18	111.5	6.7	610	2	A36116	prolactin receptor
19	111	6.7	279	2	B32985	somatotropin-bindi
20	111	6.7	638	2	A33505	somatotropin recep
21	109.5	6.6	462	1	A37986	interleukin-6 rece
22	108.5	6.6	1197	2	T30581	neural cell adhesi
23	108	6.5	581	2	I45971	prolactin receptor
24	107.5	6.5	638	2	S12136	somatotropin recep
25	106	6.4	288	2	B59405	prolactin receptor
26	106	6.4	376	2	A59405	prolactin receptor
27	106	6.4	622	2	A40144	prolactin receptor
28	106	6.4	1323	2	PN0568	connectin 3B - chi
29	104.5	6.3	638	2	B28176	somatotropin recep
30	104.5	6.3	677	2	S33608	somatotropin-bindi
31	104.5	6.3	978	1	A49814	protein-tyrosine k
32	103	6.2	616	2	A30304	prolactin receptor
33	102.5	6.2	579	2	B45266	MPL-K protein prec
34	102.5	6.2	635	2	A45266	MPL-P protein prec
35	102	6.2	292	2	I77525	prolactin receptor
36	102	6.2	303	2	I77524	prolactin receptor
37	102	6.2	608	2	I53269	prolactin receptor
38	102	6.2	7962	2	I38346	elastic titin - hu
39	101	6.1	696	2	G71620	hypothetical prote
40	100.5	6.1	1232	2	T43027	neural cell adhesi
41	99.5	6.0	1825	2	C88400	protein H19M22.1 [
42	99.5	6.0	1825	2	T32828	hypothetical prote
43	98.5	6.0	468	2	A45268	interleukin-9 rece
44	98.5	6.0	608	2	S32823	somatotropin recep
45	97.5	5.9	630	2	I51086	prolactin receptor

ALIGNMENTS

RESULT 1
A38957
interleukin 12B precursor [validated] - human
N;Alternate names: cytotoxic lymphocyte maturation factor 40K chain; natural killer c
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Nov-2000
C;Accession: A38957; B39359; S21688; B36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric
A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: A38957
A;Molecule type: mRNA
A;Residues: 1-328 <WOL>
A;Cross-references: GB:M65290
R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nab
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactiv
A;Reference number: A39359; MUID:91239523; PMID:1674604
A;Accession: B39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-328 <GUB>
A;Cross-references: GB:M65272; GB:M38444; NID:g180625; PIDN:AAA35695.1; PID:g180626
R;Podlaski, F.J.; Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Levin, W.; Danho, W.; Chi
Arch. Biochem. Biophys. 294, 230-237, 1992
A;Title: Molecular characterization of interleukin 12.
A;Reference number: S21688; MUID:92198015; PMID:1347984
A;Accession: S21688
A;Molecule type: protein
A;Residues: 23-28;46-59;74-80,'X',94-130;161-169,'X',171-180;213-235;240-250;289-299,
A;Experimental source: lymphoblastoid cell line NC-37
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lympho
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: B36055
A;Molecule type: protein
A;Residues: 23-45 <STE>
A;Experimental source: lymphoblastoid cell line NC-37
C;Genetics:
A;Gene: GDB:IL12B; NKSF2
A;Cross-references: GDB:127870; OMIM:161561
A;Map position: 5q31.1-5q33.1
C;Keywords: cytokine; glycoprotein; heparin binding; heterodimer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-328/Product: interleukin 12B #status predicted <MAT>
F;27-30/Region: heparin binding #status predicted
F;125/Binding site: carbohydrate (Asn) (covalent) #status absent
F;135,303/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222/Binding site: carbohydrate (Asn) (covalent) #status experimental

```
F;319/Modified site: 2'-mannosyl-tryptophan (Trp) (partial) #status experimental

  Query Match            85.8%;  Score 1418.5;  DB 2;  Length 328;
  Best Local Similarity  85.0%;  Pred. No. 1e-107;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: ||||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 2
I72789
interleukin 12 p40 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I72789
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.;
J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I72789
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-335 <RES>
A;Cross-references: GB:M86671; NID:g293663; PIDN:AAA39296.1; PID:g293664

  Query Match            64.0%;  Score 1058.5;  DB 2;  Length 335;
  Best Local Similarity  65.0%;  Pred. No. 1.9e-78;
  Matches  204;  Conservative   35;  Mismatches   62;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| |||||||||| |   |:|||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:|||||: ::|  : |||||::|||||||||||||| |||:||||||: |||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| |.:: | |  : |       |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
              ||:|| | || | |
Db        318 YYNSSCSKWACVPC 331


RESULT 3
A41242
interleukin-6 receptor precursor - human
N;Contains: interleukin-6 receptor, soluble form
C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change 21-Jul-2000
C;Accession: A41242; JU0080; S17468; A61459; S14621
R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi,
Science 241, 825-828, 1988
A;Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor
A;Reference number: A41242; MUID:88305347; PMID:3136546
A;Accession: A41242
A;Molecule type: mRNA
A;Residues: 1-468 <YAM>
A;Cross-references: GB:M20566; NID:g33845; PIDN:CAA31312.1; PID:g33846
R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi,
Proc. Jpn. Acad. 64, 209-211, 1988
A;Title: Molecular structure of interleukin 6 receptor.
A;Reference number: JU0080
A;Accession: JU0080
A;Molecule type: mRNA
A;Residues: 1-468 <YA2>
R;Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinr
Biochem. J. 277, 659-664, 1991
A;Title: Structural and functional studies on the human hepatic interleukin-6 recepto
A;Reference number: S17468; MUID:91336983; PMID:1872801
A;Accession: S17468
A;Molecule type: mRNA
A;Residues: 1-468 <SCH>
A;Cross-references: EMBL:X58298; NID:g32580; PIDN:CAA41231.1; PID:g32581
A;Experimental source: hepatoma cell line HepG2
R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.
J. Exp. Med. 170, 1409-1414, 1989
A;Title: Soluble cytokine receptors are present in normal human urine.
A;Reference number: A61459; MUID:90010793; PMID:2529343
A;Accession: A61459
A;Molecule type: protein
A;Residues: 20-49 <NOV>
C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, an
C;Comment: This growth factor receptor does not have a tyrosine kinase domain.
C;Genetics:
A;Gene: GDB:IL6R
A;Cross-references: GDB:127966; OMIM:147880
A;Map position: 1q21-1q21
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-468/Product: interleukin-6 receptor #status predicted <MAT>
F;20-363/Domain: extracellular #status predicted <EXT>
F;40-98/Domain: immunoglobulin homology <IMM2>
F;121-309/Domain: cytokine receptor homology <CRS>
F;364-386/Domain: transmembrane #status predicted <TMM>
F;387-468/Domain: intracellular #status predicted <INT>
F;47-96/Disulfide bonds: #status predicted
F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            11.7%;  Score 193;  DB 1;  Length 468;
  Best Local Similarity  22.2%;  Pred. No. 6.2e-08;
  Matches   69;  Conservative   59;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         20 PGEMVVLTCHTPEEDD---ITW------TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK 70
              ||: | |||   | :|   : |        :  |   | |: | ::  :  |:| |:|::
Db         39 PGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR 98

Qy         71 GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW-------L 123
                |:      ||:          |:  |: :      | |  |:      | |      |
Db         99 AGRPAGTVHLLV----------DVPPEEPQ------LSCFRKSPLSNVVCEWGPRSTPSL 142

Qy        124 T--AISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS---AC 178
              |  |:    ||    :  | :|    |                    :|: | |: |   |
```

```
Db        143 TTKAVLLVRKFQNSPAEDFQEP----C------------------QYSQESQKFSCQLAV 180

Qy        179 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEY 237
              |  : |  |  :  |        : | :|    |::|||| |: :  : :| | : |:|:
Db        181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240

Qy        238 PDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDA------KIRVQARD 291
              | :|::  |:: | | :: : : ::     :  |     |:   ||       ::::|::
Db        241 PHSWNS--SFYRLRFELRYRAERSKTFTTWMVKDLQHHCVI--HDAWSGLRHVVQLRAQE 296

Qy        292 RYYSSSWSDWA 302
              :    ||:|:
Db        297 EFGQGEWSEWS 307


RESULT 4
S60614
growth promoting activity receptor alpha precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S60614
R;Heller, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer, H.
Development 121, 2681-2693, 1995
A;Title: Analysis of function and expression of the chick GPA receptor (GPARalpha) sugge
A;Reference number: S60614; MUID:95401882; PMID:7671828
A;Accession: S60614
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-362 <HEL>
A;Cross-references: EMBL:Z48168; NID:g971417; PIDN:CAA88184.1; PID:g3063774
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoq
C;Keywords: growth factor receptor
F;2-89/Domain: immunoglobulin homology <IMM>
F;114-294/Domain: cytokine receptor homology <CRS>

  Query Match             10.8%;  Score 178;  DB 2;  Length 362;
  Best Local Similarity   23.9%;  Pred. No. 7.4e-07;
  Matches   73;  Conservative   48;  Mismatches  112;  Indels   72;  Gaps   14;

Qy         21 GEMVVLTCHTPEED-DITWTSAQSSEVLGS---GKTLTIQVKEFGDAGQYTCHKGGKVLS 76
              |  | : | : : |  :|| |  :::  |    |  | ::  :   :|||:|::|
Db         37 GADVTMKCGSMDWDAAVTWT-ANGTDIDDSHLNGSYLILKNVDLTQSGQYSCYEGSS--- 92

Qy         77 RSLLLIHKKEDGIWSTDILKEQKESK-----NKIFLKCEAKNYSGRFTCWWLTAISTDLK 131
                          |    || |   :       :  | | : ||   | | |     | :
Db         93 -------------WH---LKYQTYLRVGVPPKEPVLMCRSNNYPKGFYCSWHLPSPTYIP 136

Qy        132 FSVKSSRGFSDPQGVTCGAVTLSAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVV 190
              |  |        | |   :  |: :   || : :|                ::  :|
Db        137 NSFNIS--------VIHGTREMVCEKDIFPKNRCHIRYL----------QLFSTVKYKVT 178

Qy        191 VDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNS-RHVEVSWEYPDTWSTPHSYFS 249
              :   : |   : | :|    |:|||| ::  ||: |: | :||||: | :|  | | |
Db        179 LTVTNALGKNSTTLTFDEFAIVKPDPPESVVAKPVPNNPRRLEVSWQNPSSWPDPES-FP 237

Qy        250 LTFCIQAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSS 297
              | | :: :          | :|:            |       |: |:| |:|     :
Db        238 LKFFLRYR---------PLILDQWQHVELSDGTSHTITDAYAGKEYIIQVAAKDNDI-GT 287

Qy        298 WSDWA 302
              ||||:
Db        288 WSDWS 292


RESULT 5
JL0144
interleukin-6 receptor precursor (clone lambda P1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0144
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle ge
A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0144
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-440 <SUG>
A;Cross-references: GB:X51976; NID:g53548; PIDN:CAA36238.1; PID:g53549
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-440/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;358-385/Domain: transmembrane #status predicted <TRA>

  Query Match             10.7%;  Score 176.5;  DB 2;  Length 440;
  Best Local Similarity   22.1%;  Pred. No. 1.3e-06;
  Matches   68;  Conservative   54;  Mismatches  120;  Indels   65;  Gaps   14;

Qy         20 PGEMVVLTCHTPE-EDDIT----WTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKV 74
              ||  | | |   |   ::|    :: :|: |   :| || ::  :  | | | |     :
Db         39 PGATVTLICPGKEAAGNVTIHWVYSGSQNREWTTTGNTLVLRDVQLSDTGDYLCSLNDHL 98

Qy         75 LSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSV 134
              :    ||:          |:  |: :     | |  ||      | |
Db         99 VGTVPLLV----------DVPPEEPK------LSCFRKNPLVNAICEW------------ 130

Qy        135 KSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVV-DA 193
                |  | |   |     | |:::   |     : | ||      |   |  :|::  |
Db        131 ---RPSSTPSPTT--KAVLFAKKINTTN-GKSDFQVPCQYSQQLKSF--SCQVEILEGDK 182

Qy        194 IHKL----------KYENYTSSFFIRDIIKPDPPTNLQLKPLK-NSRHVEVSWEYPDTWS 242
              :: :             ::  :|    :::|||| || :  :    | ::|||::|:||
Db        183 VYHIVSLCVANSVGSKSSHNEAFHSLKMVQPDPPANLVVSAIPGRPRWLKVSWQHPETWD 242

Qy        243 TPHSYFSLTFCIQAQGKNNREKKDRL-------CVDKTSAKVVCHKDAKIRVQARDRYYS 295
              ||: | | :: :   ::|    |       ||   : : | |    ::|: ::
Db        243 P--SYYLLQFQLRYRPVWSKEFTVLLLPVAQYQCVIHDALRGVKH---VVQVRGKEELDL 297

Qy        296 SSWSDWA 302
                ||:|:
Db        298 GQWSEWS 304


RESULT 6
JL0145
interleukin-6 receptor precursor (clone lambda 301) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0145; S14543
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto,
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle
A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0145
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-460 <SUG>
A;Cross-references: GB:X51975; NID:g49725; PIDN:CAA36237.1; PID:g49726
A;Experimental source: clone lambda 301
R;Fiorillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL Data Library, July 1990
A;Description: Cloning and expression of murine IL-6 receptor.
A;Reference number: S14543
A;Accession: S14543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373,'R',375-460 <FIO>
A;Cross-references: EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-460/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
```

```
F;117-306/Domain: cytokine receptor homology <CRS>
F;358-385/Domain: transmembrane #status predicted <TRA>

  Query Match            10.7%;  Score 176.5;  DB 2;  Length 460;
  Best Local Similarity   22.1%;  Pred. No. 1.3e-06;
  Matches   68;  Conservative   54;  Mismatches  120;  Indels   65;  Gaps   14;

Qy         20 PGEMVVLTCHTPE-EDDIT----WTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKV 74
              ||  | | |   |   ::|    :: :|: |   :| || ::  :  | | | |     :
Db         39 PGATVTLICPGKEAAGNVTIHWVYSGSQNREWTTTGNTLVLRDVQLSDTGDYLCSLNDHL 98

Qy         75 LSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSV 134
              :   ||:          |:  |: :      | |  ||      | |
Db         99 VGTVPLLV----------DVPPEEPK------LSCFRKNPLVNAICEW------------ 130

Qy        135 KSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVV-DA 193
                | | |   |     | |:::   |     : | ||      |   |  :|::  |
Db        131 ---RPSSTPSPTT--KAVLFAKKINTTN-GKSDFQVPCQYSQQLKSF--SCQVEILEGDK 182

Qy        194 IHKL----------KYENYTSSFFIRDIIKPDPPTNLQLKPLK-NSRHVEVSWEYPDTWS 242
              :: :            ::  :|    :::|||| || :  :    | ::|||::|:||
Db        183 VYHIVSLCVANSVGSKSSHNEAFHSLKMVQPDPPANLVVSAIPGRPRWLKVSWQHPETWD 242

Qy        243 TPHSYFSLTFCIQAQGKNNREKKDRL-------CVDKTSAKVVCHKDAKIRVQARDRYYS 295
                ||: | | :: :   ::|    |        ||   : : | |    ::|: ::
Db        243 P--SYYLLQFQLRYRPVWSKEFTVLLLPVAQYQCVIHDALRGVKH---VVQVRGKEELDL 297

Qy        296 SSWSDWA 302
                ||:|:
Db        298 GQWSEWS 304


RESULT 7
I58141
ciliary neurotrophic factor receptor alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C;Accession: I58141; A47387
R;Ip, N.Y.; McClain, J.; Barrezueta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, S.J.
Neuron 10, 89-102, 1993
A;Title: The alpha component of the CNTF receptor is required for signaling and defines
A;Reference number: I58141; MUID:93152175; PMID:8381290
A;Accession: I58141
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-372 <IPN>
A;Cross-references: GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056
R;Clatterbuck, R.E.; Price, D.L.; Koliatsos, V.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993
A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
A;Reference number: A47387; MUID:93211934; PMID:8460125
A;Accession: A47387
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 185-260,'D',262-277 <CLA>
A;Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A;Experimental source: Sprague-Dawley, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:128471, NCBIP:128472)
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: growth factor receptor
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>

  Query Match            10.5%;  Score 173;  DB 2;  Length 372;
  Best Local Similarity   23.6%;  Pred. No. 2e-06;
  Matches   71;  Conservative   44;  Mismatches  122;  Indels   64;  Gaps   13;

Qy         21 GEMVVLTCHTPEED-DITW--TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSR 77
              |  | | | |   |  :||       :  | :|  | ::  | | :| | |       |
Db         39 GTDVTLPCGTASWDAAVTWRVNGTDLAPDLLNGSQLILRSLELGHSGLYACFHRDSWHLR 98

Qy         78 SLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--KFSVK 135
                :|:|    |:              :  | | :  |   | | |  :  | :  |:|
Db         99 HQVLLHV---GL----------PPREPVLSCRSNTYPKGFYCSWHLSAPTYIPNTFNVT 144

Qy        136 SSRGFSDPQGVTCGAVTLSAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAI 194
                      |  |:  :  |:  : || : :|          ::  :| :
Db        145 ----------VLHGSKMMVCEKDPALKNRCHIRYM----------HLFSTIKYKVSISVS 184

Qy        195 HKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYFSLTFC 253
              : | :     :|    |:|||| |:  :|:  | | :||:|: | ||  | | | | |
Db        185 NALGHNTTAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPES-FPLKFF 243

Qy        254 IQAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSSWSDW 301
              :: :          | :|:            |       |:  |:| |:|     :||||
Db        244 LRYR---------PLILDQWQHVELSNGTAHTITDAYAGKEYIIQVAAKDNEI-GTWSDW 293

Qy        302 A 302
              :
Db        294 S 294


RESULT 8
UHHUCN
ciliary neurotrophic factor receptor alpha precursor - human
N;Alternate names: CNTF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A40854; A56526
R;Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.E.; Squinto, S.P.; Y
Science 253, 59-63, 1991
A;Title: The receptor for ciliary neurotrophic factor.
A;Reference number: A40854; MUID:91289158; PMID:1648265
A;Accession: A40854
A;Molecule type: mRNA
A;Residues: 1-372 <DAV>
A;Cross-references: GB:M73238
R;Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.I.; McClai
Genomics 25, 157-163, 1995
A;Title: Genomic organization and chromosomal localization of the human and mouse gen
A;Reference number: A56526; MUID:95293367; PMID:7774913
A;Accession: A56526
A;Molecule type: DNA
A;Residues: 1-346,'S',348-372 <VAL>
A;Cross-references: GB:L38025; NID:g608654; PIDN:AAA91337.1; PID:g608656
C;Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylino
C;Comment: The CNTF receptor sequence appears to contain several PEST regions.
C;Genetics:
A;Gene: GDB:CNTFR
A;Cross-references: GDB:134652; OMIM:118946
A;Map position: 9p13-9p13
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: glycoprotein; growth factor receptor; membrane protein; phosphatidylinosi
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>
F;46-89/Disulfide bonds: #status predicted
F;60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            10.3%;  Score 170;  DB 1;  Length 372;
  Best Local Similarity   23.0%;  Pred. No. 3.4e-06;
  Matches   69;  Conservative   42;  Mismatches  127;  Indels   62;  Gaps   12;

Qy         21 GEMVVLTCHTPEED-DITW--TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSR 77
              |  | | | |   |  :||       :  | :|  | :   | | :| | |       |
Db         39 GSDVTLPCGTANWDAAVTWRVNGTDLAPDLLNGSQLVLHGLELGHSGLYACFHRDSWHLR 98

Qy         78 SLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--KFSVK 135
                :|:|    |:              :  | | :  |   | | |     | :  |:|
Db         99 HQVLLHV---GL----------PPREPVLSCRSNTYPKGFYCSWHLPTPTYIPNTFNVT 144

Qy        136 SSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIH 195
                |          : :  :   : || : :|          ::  :| :   :
Db        145 VLHG---------SKIMVCEKDPALKNRCHIRYM----------HLFSTIKYKVSISVSN 185
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Qy        196 KLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYFSLTFCI 254
Db        186 ALGHNATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPES-FPLKFFL 244

Qy        255 QAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSSWSDWA 302
Db        245 RYR---------PLILDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKDNEI-GTWSDWS 294


RESULT 9
I37891
interleukin-11 receptor alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Dec-1999
C;Accession: I37891; G01970; G01971
R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minvielle,
Blood 86, 2534-2540, 1995
A;Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic cyt
A;Reference number: I37891; MUID:95399754; PMID:7670098
A;Accession: I37891
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <RES>
A;Cross-references: EMBL:Z38102; NID:g995653; PIDN:CAA86224.1; PID:g995654
R;Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08959
A;Accession: G01970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <VAN>
A;Cross-references: EMBL:U32323; NID:g975334; PIDN:AAB36491.1; PID:g975335
R;Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08961
A;Accession: G01971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <VA2>
A;Cross-references: EMBL:U32324; NID:g975336; PIDN:AAB36492.1; PID:g975337
C;Genetics:
A;Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
F;120-310/Domain: cytokine receptor homology <CRS>

  Query Match             9.0%;  Score 149.5;  DB 2;  Length 422;
  Best Local Similarity   20.3%;  Pred. No. 0.00019;
  Matches   64;  Conservative   44;  Mismatches  143;  Indels   65;  Gaps   12;

Qy         15 WHPDA-----PGEMVVLTC-HTPEEDDITWTSAQSSEVL-----GSGKTLTIQVKEFGDA 63
Db         30 WGPPGVQYGQPGRSVKLCCPGVTAGDPVSWFRDGEPKLLQGPDSGLGHELVLAQADSTDE 89

Qy         64 GQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW- 122
Db         90 GTYIC---------------QTLDGALGGTVTLQLGYPPARPVVSCQAADYE-NFSCTWS 133

Qy        123 -----------LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY-KKYTV 170
Db        134 PSQISGLPTRYLTSYRKKTVLGADSQRRSPSTGPWPCPQDPLGAARCVVHGAEFWSQYRI 193

Qy        171 ECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKN-SR 229
Db        194 NVTEVNPLGASTRLLDVS------------------LQSILRPDPPQGLRVESVPGYPR 234

Qy        230 HVEVSWEYPDTW-STPHSYFSLTFCIQAQGKNNR--EKKDRLCVDKTSAKVVCHKDAKIR 286
Db        235 RLRASWTYPASWPCQPH--FLLKFRLQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVR 292

Qy        287 VQARDRYYSSSWSDWA 302
Db        293 VSARDFLDAGTWSTWS 308


RESULT 10
I48343
interleukin-11 receptor alpha-chain precursor - mouse
N;Alternate names: cytokine type 1 receptor
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Jan-2000
C;Accession: I48343; S51619
R;Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gos
Dev. Biol. 166, 521-542, 1994
A;Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embry
A;Reference number: I48343
A;Accession: I48343
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-432 <RES>
A;Cross-references: EMBL:X74953; NID:g673437; PIDN:CAA52908.1; PID:g673438
R;Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M
EMBO J. 13, 4765-4775, 1994
A;Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for hi
A;Reference number: S51619; MUID:95045367; PMID:7957045
A;Accession: S51619
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432 <HIL>
A;Cross-references: EMBL:U14412; NID:g576454; PIDN:AAA53248.1; PID:g576455
C;Genetics:
A;Gene: Et12/IL11
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor
F;120-310/Domain: cytokine receptor homology <CRS>

  Query Match             8.9%;  Score 146.5;  DB 2;  Length 432;
  Best Local Similarity   20.9%;  Pred. No. 0.00034;
  Matches   68;  Conservative   44;  Mismatches  130;  Indels   83;  Gaps   14;

Qy         15 WHPDA-----PGEMVVLTC-----HTPEEDDITWTSAQSSEVL-----GSGKTLTIQVKE 59
Db         30 WGPPGVQYGQPGRPVMLCCPGVSAGTP----VSWFRDGDSRLLQGPDSGLGHRLVLAQVD 85

Qy         60 FGDAGQYTCH-----KGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNY 114
Db         86 SPDEGTYVCQTLDGVSGGMVTLKLGFPPARPE-------------------VSCQAVDY 125

Qy        115 SGRFTCWW-----------LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDN 162
Db        126 E-NFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQRESPSTGPWPCPQDPLEASRCVVHG 184

Qy        163 RDY-KKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 221
Db        185 AEFWSEYRINVTEVNPLGASTCLLDVR------------------LQSILRPDPPQGLR 225

Qy        222 LKPLKN-SRHVEVSWEYPDTW-STPHSYFSLTFCIQAQGKNNR--EKKDRLCVDKTSAKV 277
Db        226 VESVPGYPRRLHASWTYPASWRRQPH--FLLKFRLQYRPAQHPAWSTVEPIGLEEVITDA 283

Qy        278 VCHKDAKIRVQARDRYYSSSWSDWA 302
Db        284 VAGLPHAVRVSARDFLDAGTWSAWS 308


RESULT 11
H96544
hypothetical protein F8A12.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96544
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
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Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-812 <STO>
A;Cross-references: GB:AE005173; NID:g11094686; PIDN:AAG29622.1; GSPDB:GN00141
C;Genetics:
A;Gene: F8A12.4
A;Map position: 1

  Query Match             8.0%;  Score 132;  DB 2;  Length 812;
  Best Local Similarity   25.0%;  Pred. No. 0.011;
  Matches   71;  Conservative   33;  Mismatches  112;  Indels   68;  Gaps   15;

Qy         26 LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKK 85
              ::| ||   | :|       |:|| |||   :   ||   :    | |:  ||
Db        426 ISCDTPMFCD-SW----RKRVVGSAKTLRTSI---GDDTSFV-PSGSKMNRRS------- 469

Qy         86 EDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--------------- 130
              |||      : |    |   |:|   ||      |      || |
Db        470 EDG----RKIAEDSTKKRLKFMKSARKNDGS--TMGQKQVISDDADDDDSLTVAQITTLY 523

Qy        131 --KFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP-SAEESLPI 187
               |:|  |    |:| |           |:  ||   :     ||: |:     :|::|
Db        524 KKKYSENSGGNASEPLG--------KKIRLEADNNGLE----PCQKLSSIRYDGDETVPP 571

Qy        188 EVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSY 247
               :     | : |   |   :| :: |   :|    |:   | :::    |:|
Db        572 PEI-----KKRNEETGSKSGMRVVLSPFDESNSSKPPVDFGRAIDIVVSAPET------- 619

Qy        248 FSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKI-RVQAR 290
              :|||    | || |||  :  |    | : |:|  | |  ||
Db        620 --MTFCDDVYG-NNAEKKTMIDDDSEELKCLLHEDGTITREMAR 660


RESULT 12
T30532
neural cell adhesion molecule L1 homolog - Fugu rubripes
C;Species: Fugu rubripes
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Mar-2002
C;Accession: T30532
R;Riboldi Tunnicliffe, G.R.; Platzer, M.; Nyakatura, G.; Elgar, G.S.; Brenner, S.; Rosen
submitted to the EMBL Data Library, September 1997
A;Description: Analysis of the genomic loci of Fugu rubripes homologs of the human disea
A;Reference number: Z20848
A;Accession: T30532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1277 <RIB>
A;Cross-references: EMBL:AF026198; NID:g3098263; PID:g3098264; PIDN:AAC15580.1
C;Genetics:
A;Introns: 42/1; 47/1; 81/2; 149/1; 190/1; 247/1; 285/2; 347/1; 391/1; 440/1; 477/2; 531
/2
A;Note: L1-CAM
C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; i

  Query Match             7.4%;  Score 122.5;  DB 2;  Length 1277;
  Best Local Similarity   22.9%;  Pred. No. 0.12;
  Matches   77;  Conservative   44;  Mismatches  122;  Indels   93;  Gaps   15;

Qy         19 APGEMVVLTCHTP--EEDDITWT------SAQSSE---VLGSGKTLTIQVKEFGDAGQYT 67
              |||| | | |         ||||      || | |    |    :| ::  ' |||   |
Db        361 APGETVKLDCQADGIPSPTITWTVNGVPLSATSLEPRRSLTESGSLILKDVIFGDTAIYQ 420

Qy         68 C---HKGGKVLSRSLLLIHK------KEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRF 118
              |   :| | :|: : : : :       |:|   | :         |  |:||
Db        421 CQASNKHGTILANTNVYVIELPPQILTENGNTYTFV------EGQKALLECETFGSPKPK 474

Qy        119 TCWWLTAIS---TDLKFSVKSSRGFS------DPQGV-TC----GAVTLSAERVRVDNRD 164
                |  ::||    | : :: :: |        | :|: ||      ::::|| | | ||
Db        475 VTWESSSISLLLADPRVNLLTNGGLEIANVSHDDEGIYTCLVQGSNISVNAE-VEVLNRT 533

Qy        165 Y----------------------------------------------KKYTVECQEGS 176
                                                            |||| :   |
Db        534 VILSPPQALRLQPGKTAIFTCLYVTDPKLSSPLLQWRKNDQKIFESHSDKKYTFD-GPGL 592

Qy        177 ACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWE 236
                : |           | ||     :|:  : |  :|||| :||:   |: | | ::|
Db        593 IISNVEPGDEGVYTCQIITKLDMVEASSTLTLCD--RPDPPVHLQVTNAKH-RVVTLNWT 649

Qy        237 YPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDK 272
               |  ::|   : : |  |   :|  |:  |:  ||
Db        650 PGDDNNSPILEYVVEFEDQDMKENGWEELKRVAADK 685


RESULT 13
JQ1655
prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
A;Molecule type: mRNA
A;Residues: 1-831 <TAN>
A;Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A;Experimental source: kidney
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

  Query Match             6.9%;  Score 114;  DB 2;  Length 831;
  Best Local Similarity   17.4%;  Pred. No. 0.34;
  Matches   50;  Conservative   44;  Mismatches  106;  Indels   88;  Gaps   10;

Qy         47 LGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTD----ILKEQKESK 102
              | :|    :||:   | |:::                          ||::    |   |   :
Db        194 LNAGMRYVVQVRCTLDPGEWS---------------------EWSSERHILIPSGQSPPE 232

Qy        103 NKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDN 162
                :|| :      |||||                                  :  :|
Db        233 KPTIIKCRSPE-KETFTCWW---------------------------------KPGLDG 257

Qy        163 RDYKKYT-VECQEGS----ACPSAEESLPIEVVVDAIHKLKYENYTSS----------- 205
                 || :  :||      ||    : |     |  |   :  |  :
Db        258 GHPTNYTLLYSKEGEEQVYECPDYRTAGPNSCYFDKKHTSFWTIYNITVRATNEMGSNSS 317

Qy        206 ----FFIRDIIKPDPPTNLQL---KPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQG 258
                  :  |::|||| |: |   ||:    :: ::|  |       : :| : :: :
Db        318 DPHYVDVTYIVQPDPPVNVTLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKP 377

Qy        259 KNNREKKDRLCVDKTSAKVVCHKDAK---IRVQARDRYYSSSWSDWAS 303
              :   | :     :|  |:      |   |::  :  ::  |||:|:|
Db        378 EEGEEWETIFVGQQTQYKMFSLNPGKKYIIQIHCKPDHH-GSWSEWSS 424


RESULT 14
I45877
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - aurochs
C;Species: Bos primigenius (aurochs)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Apr-2000
C;Accession: I45877
R;Kubota, T.; Hikono, H.; Sasaki, E.; Sakurai, M.
Gene 141, 305-306, 1994
```

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A;Title: Sequence of a bovine c-kit proto-oncogene cDNA.
A;Reference number: I45877; MUID:94215924; PMID:7512939
A;Accession: I45877
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-977 <KUB>
A;Cross-references: GB:D16680; NID:g516659; PIDN:BAA04084.1; PID:g516660
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;329-395/Domain: immunoglobulin homology <IMM>
F;588-932/Domain: protein kinase homology <KIN>

  Query Match             6.9%;  Score 114;  DB 2;  Length 977;
  Best Local Similarity   26.4%;  Pred. No. 0.41;
  Matches   59;  Conservative   36;  Mismatches   74;  Indels   82;  Gaps   21;

Qy         16 HPDAPGEMVV-------LTCHTPEEDDITWTSAQSSEVLG--SGKTLTIQVKEFGDA--- 63
              || |  |::|       | |  |    : ||     |:||  | ||    :  |  :|
Db         40 HP-AKSELIVSVGDEIRLLCTDP--GFVKWT----FEILGQLSEKTNPEWITEKAEATNT 92

Qy         64 GQYTC-HKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKC-----EAKNYSGR 117
              | ||| :|||  || |: :  :  : ::  |:    || :|   ::|     |  {||
Db         93 GNYTCTNKGG--LSSSIYVFVRDPEKLFLIDLPLYGKE-ENDTLVRCPLTDPEVTNYS-- 147

Qy        118 FTCWWLTA-----ISTDLKFSVKSSRGFSDPQ-GVTCGAVTLSAERVRVDNRDYKKYTVE 171
                   ||       :  || |         :||: |:|          :|   |:| :  :
Db        148 -----LTGCEGKPLPKDLTF-------VADPKAGIT----------IRNVKREYHRLCLH 185

Qy        172 C---QEGSACPSAEESLPIEVVVDA-----IHKLKY-----ENYTSSFFIRDI------- 211
              |   | | :  | : :| :   : |     : |  |     | :  :  |:|:
Db        186 CSANQRGKSMLSKKFTLKVRAAIKAVPVVSVSKTSYLLREGEEFAVTCLIKDVSSSVDSM 245

Qy        212 -IKPD-PPTNLQLKPLKNSRH 230
               || :   |  | |  ||| |
Db        246 WIKENSQQTKAQTK--KNSWH 264


RESULT 15
A29884
prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C;Accession: A29884
R;Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville
Cell 53, 69-77, 1988
A;Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
A;Reference number: A29884; MUID:88165059; PMID:2832068
A;Accession: A29884
A;Molecule type: mRNA
A;Residues: 1-310 <BOU>
A;Cross-references: GB:M19304; NID:g206364; PIDN:AAA41937.1; PID:g206365
C;Superfamily: cytokine receptor homology
C;Keywords: transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-310/Product: prolactin receptor #status predicted <MAT>
F;31-216/Domain: cytokine receptor homology <CRS>

  Query Match             6.7%;  Score 111.5;  DB 2;  Length 310;
  Best Local Similarity   21.9%;  Pred. No. 0.15;
  Matches   51;  Conservative   42;  Mismatches   99;  Indels   41;  Gaps   10;

Qy         89 IWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTC 148
              : :  :|{ |          || : :    ||||      ||        |  :|
Db         11 VLNISLLKGQSPPGKPEIHKCRSPD-KETFTCWWNP--GTDGGLPTNYSLTYS------- 60

Qy        149 GAVTLSAERVRVDNRDYKKYTVECQE-----GSACPSAEESLPI-EVVVDAIHKLKYENY 202
                        :: :| | || :        ::|  :::   | :: :  ::
Db         61 --------------KEGEKTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGS 106

Qy        203 TSS----FFIRDIIKPDPPTN--LQLKPLKNSR-HVEVSWEYPDTWSTPHSYFSLTFCIQ 255
              :||      :  |::|:|| |  |::| ||: : :: | |  |        :|:: : |:
Db        107 SSSDPLYVDVTYIVEPEPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIR 166

Qy        256 AQGKNNREKKDRLCVDKTSAKVV-CHKDAKIRVQAR---DRYYSSSWSDWASV 304
                 : :   | :       :|  ||    :   |  || |   |  | | ||  :||
Db        167 LKPEEAEEWEIHFTGHQTQFKVFDLYPGQKYLVQTRCKPDHGYWSRWSQESSV 219


Search completed: July 15, 2003, 11:08:43
Job time : 15.4559 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:28 ; Search time 6.72797 Seconds
(without alignments)
1892.583 Million cell updates/sec

Title: US-09-917-265-53
Perfect score: 1653
Sequence: 1 IWELEKDVYVVELDWHPDAP.....QARDRYYSSSWSDWASVSCS 307

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1652	99.9	329	1	I12B_CANFA	Q28268 canis famil
2	1546	93.5	329	1	I12B_FELCA	O02744 felis silve
3	1469	88.9	329	1	I12B_HORSE	Q9xsq5 equus cabal
4	1427	86.3	327	1	I12B_CEREL	Q28234 cervus elap
5	1418.5	85.8	328	1	I12B_HUMAN	P29460 homo sapien
6	1411	85.4	327	1	I12B_BOVIN	P46282 bos taurus
7	1407	85.1	327	1	I12B_SHEEP	O02815 ovis aries
8	1406.5	85.1	328	1	I12B_MACMU	P48095 macaca mula
9	1389.5	84.1	324	1	I12B_PIG	Q28938 sus scrofa
10	1368.5	82.8	328	1	I12B_CERTO	P46658 cercocebus
11	1255	75.9	327	1	I12B_MARMO	Q61729 marmota mon
12	1058.5	64.0	335	1	I12B_MOUSE	P43432 mus musculu
13	193	11.7	468	1	IL6A_HUMAN	P08887 homo sapien
14	178	10.8	362	1	CNTR_CHICK	P51641 gallus gall
15	176.5	10.7	460	1	IL6A_MOUSE	P22272 mus musculu
16	173	10.5	372	1	CNTR_RAT	Q08406 rattus norv
17	171.5	10.4	467	1	IL6A_PIG	O18796 sus scrofa
18	170	10.3	372	1	CNTR_HUMAN	P26992 homo sapien
19	157.5	9.5	462	1	IL6A_RAT	P22273 rattus norv
20	116.5	7.0	978	1	KIT_FELCA	Q28889 felis silve
21	114	6.9	831	1	PRLR_CHICK	Q04594 gallus gall
22	114	6.9	977	1	KIT_BOVIN	P43481 bos taurus
23	111.5	6.7	610	1	PRLR_RAT	P05710 rattus norv
24	111	6.7	638	1	GHR_RAT	P16310 rattus norv
25	111	6.7	978	1	KIT_CAPHI	Q28317 capra hircu
26	110	6.7	611	1	GHR_COLLI	Q90375 columba liv
27	108	6.5	581	1	PRLR_BOVIN	Q28172 bos taurus
28	107.5	6.5	638	1	GHR_PIG	P19756 sus scrofa
29	106	6.4	622	1	PRLR_HUMAN	P16471 homo sapien
30	105	6.4	581	1	PRLR_SHEEP	O46561 ovis aries
31	105	6.4	831	1	PRLR_MELGA	Q91094 meleagris g
32	104.5	6.3	638	1	GHR_RABIT	P19941 oryctolagus
33	104.5	6.3	650	1	GHR_MOUSE	P16882 mus musculu
34	103	6.2	616	1	PRLR_RABIT	P14787 oryctolagus
35	102.5	6.2	635	1	TPOR_HUMAN	P40238 homo sapien
36	102	6.2	608	1	PRLR_MOUSE	Q08501 mus musculu
37	101	6.1	975	1	KIT_CANFA	O97799 canis famil
38	98.5	6.0	468	1	IL9R_MOUSE	Q01114 mus musculu
39	98.5	6.0	608	1	GHR_CHICK	Q02092 gallus gall
40	98	5.9	581	1	PRLR_CEREL	Q28235 cervus elap
41	97.5	5.9	630	1	PRLR_ORENI	Q91513 oreochromis
42	97	5.9	975	1	KIT_MOUSE	P05532 mus musculu
43	96.5	5.8	739	1	VCA1_RAT	P29534 rattus norv
44	95	5.7	638	1	GHR_HUMAN	P10912 homo sapien
45	94	5.7	662	1	I12R_HUMAN	P42701 homo sapien

ALIGNMENTS

```
RESULT 1
I12B_CANFA
ID   I12B_CANFA     STANDARD;      PRT;   329 AA.
AC   Q28268;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98280561; PubMed=9617567;
RA   Buettner M., Belke-Louis G.F., Rziha H.J., McInnes C., Kaaden O.R.;
RT   "Detection, cDNA cloning and sequencing of canine interleukin 12.";
RL   Cytokine 10:241-248(1998).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U49100; AAA92059.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    321       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   329 AA;  37410 MW;  79F83ED02B5DA93C CRC64;

  Query Match             99.9%;  Score 1652;  DB 1;  Length 329;
  Best Local Similarity   99.7%;  Pred. No. 1.5e-129;
  Matches  306;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCVQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 2
I12B_FELCA
ID   I12B_FELCA     STANDARD;      PRT;   329 AA.
AC   O02744; O46671;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97246745; PubMed=9089110;
RA   Schijns V.E.C.J., Wierda C.M.H., Vahlenkamp T.W., Horzinek M.C.;
RT   "Molecular cloning of cat interleukin-12.";
RL   Immunogenetics 45:462-463(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98182592; PubMed=9522125;
RA   Fehr D., Dean G.A., Huder J., Fan Z., Huettner S., Higgins J.W.,
RA   Pedersen N.C., Lutz H.;
RT   "Nucleotide and predicted peptide sequence of feline interleukin-12
RT   (IL-12).";
RL   DNA Seq. 8:77-82(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y07762; CAA69068.1; -.
DR   EMBL; U83184; AAB93835.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    321       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    11     11       L -> F (IN REF. 2).
FT   CONFLICT    51     51       N -> D (IN REF. 2).
FT   CONFLICT   167    167       E -> G (IN REF. 2).
SQ   SEQUENCE   329 AA;  37374 MW;  12A069BC6322AE08 CRC64;

  Query Match             93.5%;  Score 1546;  DB 1;  Length 329;
  Best Local Similarity   93.5%;  Pred. No. 9.1e-121;
  Matches  287;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||||||||||||||:|||||||||| ||||||||||||||||||||
Db         23 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||:||| | ||||||||||||||:||||||||||||||||||||||||||||
Db         83 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||:|||||| |||| ||||| |||||:|||||||||||||||||||||:
Db        143 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||:
Db        263 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 3
I12B_HORSE
ID   I12B_HORSE     STANDARD;      PRT;   329 AA.
AC   Q9XSQ5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20009534; PubMed=10541814;
RA   Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA   Argyle D.J., Onions D.E.;
RT   "Cloning and sequencing of horse interleukin-12 and interleukin-18
RT   cDNAs.";
RL   Immunogenetics 50:94-97(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11129; CAA72011.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      236    319       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   329 AA;  37442 MW;  7104BB0DFF8FA73C CRC64;

  Query Match             88.9%;  Score 1469;  DB 1;  Length 329;
  Best Local Similarity   87.6%;  Pred. No. 2.2e-114;
  Matches  269;  Conservative   20;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||:|||||||||||||:||||: |||||||:||||||||||||||||
Db         23 IWELEKDVYVVELDWYPDAPGEMVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||| |||||||:||| | ||:||||||||||||||:||||||| ||||||||||||||
Db         83 GDAGWYTCHKGGEVLSHSHLLLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||||||||| |||:|||||| ||||||| ||:|:|||||||||||||||:
Db        143 WWLTAISTDLKFSVKSSRGSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPA 202

Qy        181 AEEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||:||||:|||||||||| |||||||||||| |||||||||| |||||||||:|
Db        203 AEESLPIEIVVDAVHKLKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPET 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| || |||| :|:|||| :|:||| | |||| :|||||||||||||||:
Db        263 WSTPHSYFSLTFSIQVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSE 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 4
I12B_CEREL
ID   I12B_CEREL     STANDARD;      PRT;   327 AA.
AC   Q28234;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99304506; PubMed=10376218;
RA   Lockhart E., Slobbe L., Buchan G.;
RT   "The characterisation of a cervine immunoregulatory cytokine,
RT   interleukin 12.";
RL   DNA Seq. 10:139-148(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U57752; AAB02258.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      236    319       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37145 MW;  53AF5BB288907F06 CRC64;

  Query Match             86.3%;  Score 1427;  DB 1;  Length 327;
  Best Local Similarity   85.7%;  Pred. No. 6.4e-111;
  Matches  263;  Conservative   21;  Mismatches   21;  Indels    2;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||:|||||| ||| | ||||| ||||| ||||||||||||||:|||||
Db         23 IWELEKNVYVVELDWYPDAPGETVVLRCDTPEEDGITWTSDQSSEVLGSGKTLTVQVKEF 82
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Qy          61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||||||:||||||||:||||||||||||||:||| | | |||||||:||| |||
Db          83 GDAGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTC 142

Qy         121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               |||||||||||||||||| |||:|||||| :|| |:| ||:|:|||||||||||||||:
Db         143 WWLTAISTDLKFSVKSSRGSSDPRGVTCGAASLSTEKVIVDHREYKKYTVECQEGSACPA 202

Qy         181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
               ||||||||||:|:|||||||||||||||||||||| ||||:|||||| ||||||||||
Db         203 AEESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDT 262

Qy         241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
               |||||||||||||:| |||| |||| | :|:||||| ||||| ||||||||||:| ||:
Db         263 WSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVTCHKDASIRVQARDRYYNSFWSE 320

Qy         301 WASVSCS 307
               |||||||
Db         321 WASVSCS 327
```

RESULT 5
I12B_HUMAN
ID I12B_HUMAN STANDARD; PRT; 328 AA.
AC P29460;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE maturation factor 40 kDa subunit) (CLMF p40) (NK cell stimulatory
DE factor chain 2) (NKSF2).
GN IL12B OR NKSF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91239523; PubMed=1674604;
RA Gubler U., Chua A.O., Schoenhaut D.S., Dwyer C.M., McComas W.,
RA Motyka R., Nabavi N., Wolitzky A.G., Quinn P.M., Familletti P.C.,
RA Gately M.K.;
RT "Coexpression of two distinct genes is required to generate secreted
RT bioactive cytotoxic lymphocyte maturation factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4143-4147(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91201875; PubMed=1673147;
RA Wolf S.F., Temple P.A., Kobayashi M., Young D., Dicig M., Lowe L.,
RA Dzialo R., Fitz L., Ferenz C., Hewick R.M., Kelleher K.,
RA Herrmann S.H., Clark S.C., Azzoni L., Chan S.H., Trinchieri G.,
RA Perussia B.;
RT "Cloning of cDNA for natural killer cell stimulatory factor, a
RT heterodimeric cytokine with multiple biologic effects on T and
RT natural killer cells.";
RL J. Immunol. 146:3074-3081(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11197695;
RA Huang D., Cancilla M.R., Morahan G.;
RT "Complete primary structure, chromosomal localization, and definition
RT of polymorphisms of the gene encoding the human interleukin 12 p40
RT subunit.";
RL Genes Immun. 1:515-520(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Hongyuan J., Meiyun Z.;
RT "Cloning and sequence analysis of IL-12 cDNA from Chinese.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE OF 23-45.
RX MEDLINE=90370873; PubMed=2204066;
RA Stern A.S., Podlaski F.J., Hulmes J.D., Pan Y.C.E., Quinn P.M.,
RA Wolitzky A.G., Familletti P.C., Stremlo D.L., Truitt T.,
RA Chizzonite R., Gately M.K.;
RT "Purification to homogeneity and partial characterization of
RT cytotoxic lymphocyte maturation factor from human B-lymphoblastoid
RT cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6808-6812(1990).
RN [6]
RP SIMILARITY TO IL-6 RECEPTOR.
RX MEDLINE=91300556; PubMed=2070420;
RA Gearing D.P., Cosman D.;
RT "Homology of the p40 subunit of natural killer cell stimulatory
RT factor (NKSF) with the extracellular domain of the interleukin-6
RT receptor.";
RL Cell 66:9-10(1991).
RN [7]
RP CARBOHYDRATE-LINKAGE SITE TRP-319.
RX MEDLINE=99225373; PubMed=10207176;
RA Doucey M.A., Hess D., Blommers M.J., Hofsteenge J.;
RT "Recombinant human interleukin-12 is the second example of a
RT C-mannosylated protein.";
RL Glycobiology 9:435-441(1999).
CC -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
CC T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC BY RESTING PBMC.
CC -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC SUBUNITS. NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE
CC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: KNOWN TO BE C-MANNOSYLATED IN THE RECOMBINANT PROTEIN; IT IS
CC NOT YET KNOWN FOR SURE IF THE WILD-TYPE PROTEIN IS ALSO MODIFIED.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC --
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CC --
DR EMBL; M65272; AAA35695.1; -.
DR EMBL; M65290; AAA59938.1; -.
DR EMBL; AY008847; AAG32620.1; -.
DR EMBL; AF180563; AAD56386.1; -.
DR PIR; B39359; B39359.
DR PIR; B36055; B36055.
DR GlycoSuiteDB; P29460; -.
DR Genew; HGNC:5970; IL12B.
DR MIM; 161561; -.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 22
FT CHAIN 23 328 INTERLEUKIN-12 BETA CHAIN.
FT DOMAIN 43 97 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 235 320 FIBRONECTIN TYPE-III.
FT DISULFID 50 90 POTENTIAL.
FT DISULFID 199 199 INTERCHAIN (PROBABLE).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .).
FT CARBOHYD 319 319 C-LINKED (MAN).
FT /FTId=CAR_000187.
FT CONFLICT 239 239 K -> N (IN REF. 2).

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SQ   SEQUENCE   328 AA;  37169 MW;  118FA801B8F5BB2F CRC64;

  Query Match             85.8%;  Score 1418.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 3.2e-110;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| |||:|||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:|||!| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 6
I12B_BOVIN
ID   I12B_BOVIN     STANDARD;      PRT;   327 AA.
AC   P46282;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Holstein; TISSUE=Lymphoid;
RX   MEDLINE=95244628; PubMed=7727547;
RA   Zarlenga D.S., Canals A., Aschenbrenner R.A., Gasbarre L.C.;
RT   "Enzymatic amplification and molecular cloning of cDNA encoding the
RT   small and large subunits of bovine interleukin 12.";
RL   Biochim. Biophys. Acta 1270:215-217(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U11815; AAA85792.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37050 MW;  D484DA36EF6F3D9F CRC64;

  Query Match             85.4%;  Score 1411;  DB 1;  Length 327;
  Best Local Similarity   84.7%;  Pred. No. 1.3e-109;
  Matches  260;  Conservative   22;  Mismatches   23;  Indels    2;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||:||||||||:|||||| |||||  |||||  ||||| ||||||||||||||||||
Db         23 MWELEKNVYVVELDWYPDAPGETVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||: |||||||:|||||||||||||||:||| | | ||||||||:||| |||
Db         83 GDAGQYTCHKGGEALSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||||||||| |||:|||||  ||||:| :::|:| |||||||||||||:
Db        143 WWLTAISTDLKFSVKSSRGSSDPRGVTCGAALLSAEKVSLEHREYNKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||| |||||:|:|||||||||||||||||||||||| ||||:|||||| ||||||||||
Db        203 AEESLLIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||:| |||| ||||  | :|:||||| ||||| :|||||||||| ||:
Db        263 WSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVTCHKDANVRVQARDRYYSSFWSE 320

Qy        301 WASVSCS 307
              |||||||
Db        321 WASVSCS 327


RESULT 7
I12B_SHEEP
ID   I12B_SHEEP     STANDARD;      PRT;   327 AA.
AC   O02815; O18989; Q9TT18;
DT   01-NOV-1997 (Rel. 35, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Ovis aries (Sheep), and
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940, 9925;
RN   [1]
RP   SEQUENCE FROM N.A., AND SUBUNIT.
RC   SPECIES=Sheep; TISSUE=Peripheral blood;
RX   MEDLINE=20480126; PubMed=11023671;
RA   Swinburne S.J., Russ G.R., Krishnan R.;
RT   "Ovine interleukin 12 has biological activity on ovine and human
RT   activated peripheral blood mononuclear cells.";
RL   Cytokine 12:1546-1552(2000).
RN   [2]
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RP   SEQUENCE FROM N.A.
RC   SPECIES=Sheep; STRAIN=Merino; TISSUE=Peripheral blood;
RX   MEDLINE=20344025; PubMed=10888112;
RA   De Rose R., Scheerlinck J.-P.Y., Casey G., Wood P.R., Tennent J.M.,
RA   Chaplin P.J.;
RT   "Ovine interleukin-12: analysis of biologic function and species
RT   comparison.";
RL   J. Interferon Cytokine Res. 20:557-564(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=C.hircus;
RA   Beyer J.C., Cheevers W.P., Kumpula-Mcwhirter N.M.;
RT   "Cloning of caprine IL-12 40 kDa subunit.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF004024; AAB61368.2; -.
DR   EMBL; AF209435; AAF20151.1; -.
DR   EMBL; AF007576; AAB62945.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       POTENTIAL.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   290    290       T -> A (IN REF. 2).
SQ   SEQUENCE   327 AA;  36936 MW;  DDCD983A10143A96 CRC64;

  Query Match            85.1%;  Score 1407;  DB 1;  Length 327;
  Best Local Similarity  85.0%;  Pred. No. 2.9e-109;
  Matches  261;  Conservative   22;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||:|:|||| ||||| ||||| ||||| ||||||||||||||||||
Db         23 IWELEKNVYVVELDWYPNAPGETVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||||||||:|||||||||||||||:||| | | |||||||:||| |||
Db         83 GDAGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||:|||||||||| |||:|||||| :||||:| :|:|:| ||||||||||||:
Db        143 SWLTAISTNLKFSVKSSRGSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||::|:|||||||||||||||||||||| ||||:|||||| ||||||||||
Db        203 AEESLPIEVVMEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||| |||| |  |:|||| ||||| |||||||||||| ||:
Db        263 WSTPHSYFSLTFCVQVQGKNKREKK--LFTDQTSAKVTCHKDANIRVQARDRYYSSFWSE 320

Qy        301 WASVSCS 307
              |||||||
Db        321 WASVSCS 327


RESULT 8
I12B_MACMU
ID   I12B_MACMU     STANDARD;      PRT;   328 AA.
AC   P48095;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19841; AAB60397.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235    320       FIBRONECTIN TYPE-III.
```

```
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     106    106       K -> I.
FT   VARIANT     206    206       L -> P.
FT   VARIANT     218    218       L -> P.
FT   VARIANT     289    289       I -> T.
FT   VARIANT     295    295       S -> P.
SQ   SEQUENCE   328 AA;  37273 MW;  A46198AAC6D2746B CRC64;

  Query Match             85.1%;  Score 1406.5;  DB 1;  Length 328;
  Best Local Similarity   84.4%;  Pred. No. 3.2e-109;
  Matches  259;  Conservative   20;  Mismatches   27;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| ||||| |||| || ||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||: || ||||:|||||||||||:||:||| ||| ||:|||||||||||||
Db         83 GDAGQYTCHKGGEALSHSLLLLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |:|||||||||||||||| ||:::| :|:|||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSNPQGVTCGAVTLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||| |||||:|||||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEERLPIEVMVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||| ||| |||||:  ||||| |:| |:|   |||:|||||||||:
Db        262 WSTPHSYFSLTFCIQVQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 9
I12B_PIG
ID   I12B_PIG       STANDARD;      PRT;   324 AA.
AC   Q28938;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=97383978; PubMed=9239844;
RA   Foss D.L., Murtaugh M.P.;
RT   "Molecular cloning and mRNA expression of porcine interleukin-12.";
RL   Vet. Immunol. Immunopathol. 57:121-134(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U08317; AAA75356.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    324       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     231    316       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   195    195       INTERCHAIN (PROBABLE).
FT   CARBOHYD   125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   218    218       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   324 AA;  36828 MW;  F0E48B72F700086C CRC64;

  Query Match             84.1%;  Score 1389.5;  DB 1;  Length 324;
  Best Local Similarity   83.4%;  Pred. No. 8e-108;
  Matches  256;  Conservative   21;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||:|:|||||||||:|||| |||| |||||||:|||||| ||||
Db         23 IWELEKNVYVVELDWYPNAPGEMVVLTCNTPEEDGITWTSDQSSEVLGTGKTLTIHVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||| ||| |||:||||:|||||||||||||||:||| ||| ||||||||||||||
Db         83 GDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQKEPKNKSFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||||||||| :||:|||||  |||       |  :|||| ||||||||||:
Db        143 WWLTAISTDLKFSVKSSRGSTDPRGVTCGTATLSE-----DLGEYKKYRVECQEGSACPA 197

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||::|:|||||||||||||||||||||||| |||| ||||||||:|||||||
Db        198 AEESLPIEVVLEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLNPLKNSRHVEISWEYPDT 257

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||| | :| |||| |||||:|  |: |||| ||||| ||||||||||||||:
Db        258 WSTPHSYFSLMFGVQVQGKNKREKKDKLFTDQISAKVTCHKDANIRVQARDRYYSSSWSE 317

Qy        301 WASVSCS 307
              |||||||
Db        318 WASVSCN 324


RESULT 10
I12B_CERTO
ID   I12B_CERTO     STANDARD;      PRT;   328 AA.
AC   P46658;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19834; AAA86701.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      235    320       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    303    303       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   328 AA;  37252 MW;  A2DE98E844435B14 CRC64;

  Query Match             82.8%;  Score 1368.5;  DB 1;  Length 328;
  Best Local Similarity   82.1%;  Pred. No. 4.4e-106;
  Matches  252;  Conservative   22;  Mismatches   32;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| ||||| |||| || ||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||: || |||| |||||||||||||:||| ||: ||:|||||||| ||
Db         83 GDAGQYTCHKGGEALSHSLLLPHKKEDGIWSTDILKDQKEPKNETFLRCEAKNYSGRITC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||: ||||| ||: |||| |:|||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLSTISTDLTFSIISSRGSSNPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||| |||||:|||||||||||||||||||||||| |||||||||| |||||||||||:::
Db        202 AEERLPIEVMVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||| ||||: ||||||:  ||||| |:| |:|   |||:||||||||::
Db        262 WSTPHSYFSLTFCIQVQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWNE 321

Qy        301 WASVSCS 307
              | || ||
Db        322 WTSVPCS 328


RESULT 11
I12B_MARMO
ID   I12B_MARMO     STANDARD;      PRT;   327 AA.
AC   Q61729;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Laxton C.D., Foster G.R., Shanmuganathan S., Mills J.S.,
RA   Ackrill A.M.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X97019; CAA65747.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      235    319       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37172 MW;  9A15445915AB90E6 CRC64;

  Query Match             75.9%;  Score 1255;  DB 1;  Length 327;
  Best Local Similarity   74.8%;  Pred. No. 1.1e-96;
  Matches  229;  Conservative   34;  Mismatches   41;  Indels    2;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||||| ||| ||||| ||||| ||||| |||||||||||||| ||||
Db         23 IWELEKNVYVVELDWHPDTPGEKVVLTCDTPEEDGITWTSEQSSEVLGSGKTLTILVKEF 82
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Qy          61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||| ||| :||:|||: |||:|| |||||||||| :|| :||  : ||||||||||
Db          83 EDAGHYTCRRGGEVLSQMLLLLHKNEDGIWSTDILK-KKEPENKNLVTCEAKNYSGRFTC 141

Qy         121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               |||||||||: ||||| || |||||||||  |||||||::: |:||||:|:||| :|||:
Db         142 WWLTAISTDVNFSVKSHRGSSDPQGVTCGEATLSAERVKIEQREYKKYSVQCQEDNACPT 201

Qy         181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
               |||:||| |||||:|||||||| |||||||||||||| ||::|| |  : |||:|||||:
Db         202 AEETLPITVVVDAVHKLKYENYISSFFIRDIIKPDPPKNLKMKPSKTPQQVEVTWEYPDS 261

Qy         241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
               |||||||||||| :| |||  ::: : | |||||  | | | ||: ||||||||:||||:
Db         262 WSTPHSYFSLTFSVQVQGK-KKKRSNTLHVDKTSVTVTCQKGAKVSVQARDRYYNSSWSE 320

Qy         301 WASVSC 306
               ||::||
Db         321 WATMSC 326


RESULT 12
I12B_MOUSE
ID   I12B_MOUSE     STANDARD;      PRT;   335 AA.
AC   P43432;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=92268481; PubMed=1350290;
RA   Schoenhaut D.S., Chua A.O., Wolitzky A.G., Quinn P.M., Dwyer C.M.,
RA   Gately M.K., Gubler U.;
RT   "Cloning and expression of murine IL-12.";
RL   J. Immunol. 148:3433-3440(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96257799; PubMed=8647196;
RA   Tone Y., Thompson S.A., Babik J.M., Nolan K.F., Tone M., Raven C.,
RA   Waldmann H.;
RT   "Structure and chromosomal location of the mouse interleukin-12 p35
RT   and p40 subunit genes.";
RL   Eur. J. Immunol. 26:1222-1227(1996).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86671; AAA39296.1; -.
DR   EMBL; S82426; AAB37383.1; -.
DR   EMBL; S82421; AAB37383.1; JOINED.
DR   EMBL; S82422; AAB37383.1; JOINED.
DR   EMBL; S82424; AAB37383.1; JOINED.
DR   EMBL; S82425; AAB37383.1; JOINED.
DR   MGD; MGI:96540; Il12b.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    335       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      233    324       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    197    197       INTERCHAIN (PROBABLE).
FT   CARBOHYD     47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    122    122       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    220    220       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DOMAIN      155    159       POLY-SER.
SQ   SEQUENCE   335 AA;  38235 MW;  19E4FA5EF0CFC82A CRC64;

  Query Match             64.0%;  Score 1058.5;  DB 1;  Length 335;
  Best Local Similarity   65.0%;  Pred. No. 2e-80;
  Matches  204;  Conservative   35;  Mismatches   62;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| |||||||||| |   |:|||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:|||||: ::|  : |||||::|||||||||||| |||:|||||: |||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |         |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
              ||:|| | || | |
Db        318 YYNSSCSKWACVPC 331


RESULT 13
IL6A_HUMAN
ID   IL6A_HUMAN     STANDARD;      PRT;   468 AA.
AC   P08887; Q16202;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)
DE   (CD126 antigen).
GN   IL6R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RX   MEDLINE=88305347; PubMed=3136546;
RA   Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA   Taniguchi T., Hirano T., Kishimoto T.;
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RT   "Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2)
RT   receptor.";
RL   Science 241:825-828(1988).
RN   [2]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RA   Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA   Taniguchi T., Hirano T., Kishimoto T.;
RT   "Molecular structure of interleukin 6 receptor.";
RL   Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RX   MEDLINE=91336983; PubMed=1872801;
RA   Schooltink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,
RA   Kishimoto T., Heinrich P.C., Rose-John S.;
RT   "Structural and functional studies on the human hepatic interleukin-6
RT   receptor. Molecular cloning and overexpression in HepG2 cells.";
RL   Biochem. J. 277:659-664(1991).
RN   [4]
RP   SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).
RX   MEDLINE=94333499; PubMed=8056053;
RA   Horiuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,
RA   Matsumoto A., Yamamoto M., Yamamoto N.;
RT   "Soluble interleukin-6 receptors released from T cell or
RT   granulocyte/macrophage cell lines and human peripheral blood
RT   mononuclear cells are generated through an alternative splicing
RT   mechanism.";
RL   Eur. J. Immunol. 24:1945-1948(1994).
RN   [5]
RP   PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX   MEDLINE=99167486; PubMed=10066782;
RA   Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,
RA   Moritz R.L., Simpson R.J.;
RT   "Disulfide bond structure and N-glycosylation sites of the
RT   extracellular domain of the human interleukin-6 receptor.";
RL   J. Biol. Chem. 274:7207-7215(1999).
RN   [6]
RP   MUTAGENESIS.
RX   MEDLINE=93223711; PubMed=8467812;
RA   Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibi M.,
RA   Taga T., Kishimoto T.;
RT   "Structure-function analysis of human IL-6 receptor: dissociation of
RT   amino acid residues required for IL-6-binding and for IL-6 signal
RT   transduction through gp130.";
RL   EMBO J. 12:1705-1712(1993).
CC   -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC       WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC       ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC       LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC       REACTIONS AND HEMATOPOIESIS.
CC   -!- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6
CC       RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.
CC   -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM).
CC       SECRETED (SHORT FORM).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL
CC       BLOOD MONONUCLEAR CELLS AND WEAKLY FOUND IN URINE AND SERUM.
CC   -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC       N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC   -!- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE
CC       BY PROTEOLYSIS.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD126 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd126.htm".
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CC   ---------------------------------------------------------------------
DR   EMBL; X12830; CAA31312.1; -.
DR   EMBL; X58298; CAA41231.1; -.
DR   EMBL; S72848; AAC60635.1; -.
DR   PIR; A41242; A41242.
DR   PIR; JU0080; JU0080.
DR   PIR; S14621; S14621.
DR   PIR; S17468; S17468.
DR   Genew; HGNC:6019; IL6R.
DR   MIM; 147880; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW   Alternative splicing; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    468       INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT   DOMAIN      20    365       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   366    386       POTENTIAL.
FT   DOMAIN     387    468       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      40    103       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID    25    193
FT   DISULFID    47     96
FT   DISULFID   121    132
FT   DISULFID   165    176
FT   CARBOHYD    55     55       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    93     93       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   221    221       N-LINKED (GLCNAC. . .).
FT   VARSPLIC   356    365       VQDSSSVPLP -> GSRRRGSCGL (IN SHORT
FT                               ISOFORM).
FT   VARSPLIC   366    468       MISSING (IN SHORT ISOFORM).
FT   MUTAGEN    121    121       C->S: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    122    122       F->A: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    132    132       C->A: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    134    134       W->L: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    140    140       P->G: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    153    153       F->L: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    165    165       C->L: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    174    174       F->L: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    176    176       C->A: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    184    184       D->T: 30% DECREASE OF LIGAND-BINDING AND
FT                               IL6 SIGNALING.
FT   MUTAGEN    190    190       V->G: 80% DECREASE OF LIGAND-BINDING AND
FT                               NO IL6 SIGNALING.
FT   MUTAGEN    193    193       C->D: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    211    211       C->A: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    217    217       D->V: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    232    232       R->S: 30% DECREASE OF LIGAND-BINDING AND
FT                               IL6 SIGNALING.
FT   MUTAGEN    233    233       W->Q: 30% DECREASE OF LIGAND-BINDING AND
FT                               INCREASE OF IL6 SIGNALING.
FT   MUTAGEN    254    254       E->A: 50% DECREASE OF LIGAND-BINDING AND
FT                               IL6 SIGNALING.
FT   MUTAGEN    277    277       C->D: 30% INCREASE OF LIGAND-BINDING AND
FT                               100% INCREASE IN IL6 SIGNALING.
FT   MUTAGEN    278    278       V->N: 50% DECREASE OF LIGAND-BINDING AND
FT                               50% INCREASE IN IL6 SIGNALING.
FT   MUTAGEN    279    279       I->D: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    280    280       H->I: NO CHANGE OF LIGAND-BINDING AND NO
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FT                                   IL6 SIGNALING.
FT   MUTAGEN      281    281       D->G: 70% DECREASE OF LIGAND-BINDING AND
FT                                   NO IL6 SIGNALING.
FT   MUTAGEN      285    285       G->D: 80% DECREASE OF LIGAND-BINDING AND
FT                                   NO IL6 SIGNALING.
FT   MUTAGEN      291    291       Q->K: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN      293    293       R->G: COMPLETE LOSS OF LIGAND-BINDING.
SQ   SEQUENCE   468 AA;  51547 MW;  62AA239FA14F1B8B CRC64;

  Query Match             11.7%;  Score 193;  DB 1;  Length 468;
  Best Local Similarity   22.2%;  Pred. No. 1.3e-08;
  Matches   69;  Conservative   59;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         20 PGEMVVLTCHTPEEDD---ITW------TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK 70
              ||: | |||   | :|   : |       :  |   | |: | ::  :  |:| |:|::
Db         39 PGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR 98

Qy         71 GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW-------L 123
               |:      ||:          |:  |: :      | |  |:      | |       |
Db         99 AGRPAGTVHLLV----------DVPPEEPQ------LSCFRKSPLSNVVCEWGPRSTPSL 142

Qy        124 T--AISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS---AC 178
               |  |:    ||    :  | :|    |                  :|: | |: |   |
Db        143 TTKAVLLVRKFQNSPAEDFQEP----C------------------QYSQESQKFSCQLAV 180

Qy        179 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEY 237
              |  : |  |  :  |       : | :|    |::|||| |: :  : :| | : |:|:
Db        181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240

Qy        238 PDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDA------KIRVQARD 291
              | :|::  |:: | | :: : : ::    :  |     |:  ||       ::::|::
Db        241 PHSWNS--SFYRLRFELRYRAERSKTFTTWMVKDLQHHCVI--HDAWSGLRHVVQLRAQE 296

Qy        292 RYYSSSWSDWA 302
              :    ||:|:
Db        297 EFGQGEWSEWS 307


RESULT 14
CNTR_CHICK
ID   CNTR_CHICK     STANDARD;      PRT;   362 AA.
AC   P51641;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ciliary neurotrophic factor receptor alpha precursor (CNTFR alpha)
DE   (Growth promoting activity receptor alpha) (GPA receptor alpha) (GPAR
DE   alpha).
GN   CNTFR.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96064819; PubMed=7595532;
RA   Ip F.C.F., Fu A.K.Y., Tsim K.W.K., Ip N.Y.;
RT   "Cloning of the alpha component of the chick ciliary neurotrophic
RT   factor receptor: developmental expression and down-regulation in
RT   denervated skeletal muscle.";
RL   J. Neurochem. 65:2393-2400(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95401882; PubMed=7671828;
RA   Heller S., Finn T.P., Huber J., Nishi R., Geissen M., Pueschel A.W.,
RA   Rohrer H.;
RT   "Analysis of function and expression of the chick GPA receptor (GPAR
RT   alpha) suggests multiple roles in neuronal development.";
RL   Development 121:2681-2693(1995).
CC   -!- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE
CC       RECEPTOR SPECIFICITY.
CC   -!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN NERVOUS SYSTEM. ALSO FOUND
CC       IN SKELETAL MUSCLE.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC   ---------------------------------------------------------------------
DR   EMBL; U29245; AAA87838.1; -.
DR   EMBL; Z48168; CAA88184.1; -.
DR   HSSP; P16471; 1BP3.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; iq; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    334       CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT                                 ALPHA.
FT   PROPEP      335    362       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       37     94       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      199    300       FIBRONECTIN TYPE-III.
FT   DISULFID     44     87       POTENTIAL.
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    188    188       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       334    334       GPI-ANCHOR (POTENTIAL).
FT   CONFLICT    337    337       A -> V (IN REF. 2).
SQ   SEQUENCE   362 AA;  40307 MW;  5A90217EB48419F7 CRC64;

  Query Match             10.8%;  Score 178;  DB 1;  Length 362;
  Best Local Similarity   23.9%;  Pred. No. 1.6e-07;
  Matches   73;  Conservative   48;  Mismatches  112;  Indels   72;  Gaps   14;

Qy         21 GEMVVLTCHTPEED-DITWTSAQSSEVLGS---GKTLTIQVKEFGDAGQYTCHKGGKVLS 76
              |  | : | : : |  :||| |  :::  |   |  | ::  :   :|||:|::|
Db         37 GADVTMKCGSMDWDAAVTWT-ANGTDIDDSHLNGSYLILKNVDLTQSGQYSCYEGSS--- 92

Qy         77 RSLLLIHKKEDGIWSTDILKEQKESK-----NKIFLKCEAKNYSGRFTCWWLTAISTDLK 131
                          |    || |   :      :  | | : ||   | | |     | :
Db         93 ------------WH---LKYQTYLRVGVPPKEPVLMCRSNNYPKGFYCSWHLPSPTYIP 136

Qy        132 FSVKSSRGFSDPQGVTCGAVTLSAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVV 190
              |   |       |  |   :  |: :  || : :|          ::  :|
Db        137 NSFNIS--------VIHGTREMVCEKDIFPKNRCHIRYL----------QLFSTVKYKVT 178

Qy        191 VDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNS-RHVEVSWEYPDTWSTPHSYFS 249
              :   : |   : | :|    |:|||||| ::  ||: |: | :|||| : :|  | | |
Db        179 LTVTNALGKNSTTLTFDEFAIVKPDPPESVVAKPVPNNPRRLEVSWQNPSSWPDPES-FP 237

Qy        250 LTFCIQAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSS 297
              | | :: :          | :|:            |       |:  |:| |:|     :
Db        238 LKFFLRYR---------PLILDQWQHVELSDGTSHTITDAYAGKEYIIQVAAKDNDI-GT 287

Qy        298 WSDWA 302
              ||||:
Db        288 WSDWS 292
```

```
RESULT 15
IL6A_MOUSE
ID   IL6A_MOUSE     STANDARD;      PRT;   460 AA.
AC   P22272;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
GN   IL6RA OR IL6R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Spleen;
RX   MEDLINE=90278354; PubMed=2112585;
RA   Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA   Kishimoto T.;
RT   "Functional murine interleukin 6 receptor with the intracisternal A
RT   particle gene product at its cytoplasmic domain. Its possible role in
RT   plasmacytomagenesis.";
RL   J. Exp. Med. 171:2001-2009(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H; TISSUE=Liver;
RA   Fiorillo M.T., Ciliberto G., Dente L.;
RL   Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC       WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC       ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC       LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC       REACTIONS AND HEMATOPOIESIS.
CC   -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC       C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X51975; CAA36237.1; -.
DR   EMBL; X53802; CAA37810.1; -.
DR   PIR; JL0144; JL0144.
DR   PIR; JL0145; JL0145.
DR   PIR; S14543; S14543.
DR   HSSP; P16471; 1BP3.
DR   MGD; MGI:105304; Il6ra.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW   Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    460       INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT   DOMAIN       20    364       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    365    385       POTENTIAL.
FT   DOMAIN      386    460       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       40     99       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     25    190       BY SIMILARITY.
FT   DISULFID     47     92       BY SIMILARITY.
FT   DISULFID    117    128       BY SIMILARITY.
FT   DISULFID    162    173       BY SIMILARITY.
FT   CARBOHYD     32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     55     55       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    150    150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    374    374       A -> R (IN REF. 2).
SQ   SEQUENCE   460 AA;  50454 MW;  F85C5906D08525C4 CRC64;

  Query Match             10.7%;  Score 176.5;  DB 1;  Length 460;
  Best Local Similarity   22.1%;  Pred. No. 2.9e-07;
  Matches   68;  Conservative   54;  Mismatches  120;  Indels   65;  Gaps   14;

Qy         20 PGEMVVLTCHTPE-EDDIT----WTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKV 74
              ||  | | |   |   ::|    :: :|: |   :| || ::  :  | | | |     :
Db         39 PGATVTLICPGKEAAGNVTIHWVYSGSQNREWTTTGNTLVLRDVQLSDTGDYLCSLNDHL 98

Qy         75 LSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSV 134
              :   ||:          |:  |: :      | |  ||      | |
Db         99 VGTVPLLV----------DVPPEEPK------LSCFRKNPLVNAICEW------------ 130

Qy        135 KSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVV-DA 193
                |  | |   |    | |:::   |    : | ||      |   |  :|::  |
Db        131 ---RPSSTPSPTT--KAVLFAKKINTTN-GKSDFQVPCQYSQQLKSF--SCQVEILEGDK 182

Qy        194 IHKL----------KYENYTSSFFIRDIIKPDPPTNLQLKPLK-NSRHVEVSWEYPDTWS 242
              :: :            ::  :|    :::|||| ||: :  :    | ::|||::|:||
Db        183 VYHIVSLCVANSVGSKSSHNEAFHSLKMVQPDPPANLVVSAIPGRPRWLKVSWQHPETWD 242

Qy        243 TPHSYFSLTFCIQAQGKNNREKKDRL-------CVDKTSAKVVCHKDAKIRVQARDRYYS 295
                ||: | | :: :   ::|    |       ||   : : | |    ::|: ::
Db        243 P--SYYLLQFQLRYRPVWSKEFTVLLLPVAQYQCVIHDALRGVKH---VVQVRGKEELDL 297

Qy        296 SSWSDWA 302
                ||:|:
Db        298 GQWSEWS 304


Search completed: July 15, 2003, 11:07:01
Job time : 7.72797 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:57:19 ; Search time 27.2044 Seconds
(without alignments)
2325.231 Million cell updates/sec

Title: US-09-917-265-53
Perfect score: 1653
Sequence: 1 IWELEKDVYVVELDWHPDAP.....QARDRYYSSSWSDWASVSCS 307

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1272.5	77.0	332	11	Q924V5	Q924v5 cavia porce
2	1268	76.7	327	11	Q9ET05	Q9et05 marmota mon
3	1208	73.1	327	11	Q91ZK7	Q91zk7 sigmodon hi
4	1063.5	64.3	335	11	Q9QUM1	Q9qum1 mus musculu
5	1060.5	64.2	335	11	Q9R278	Q9r278 rattus norv
6	944	57.1	195	6	Q95N82	Q95n82 canis famil
7	940	56.9	268	11	Q62712	Q62712 rattus norv
8	927.5	56.1	344	11	Q924K7	Q924k7 meriones un
9	818	49.5	174	6	Q28232	Q28232 cervus elap
10	799	48.3	150	6	Q9BG70	Q9bg70 canis famil
11	768	46.5	149	6	Q9TV09	Q9tv09 canis famil
12	727.5	44.0	169	11	Q9Z1Y8	Q9z1y8 cavia porce
13	695	42.0	143	6	O62779	O62779 felis silve
14	507	30.7	132	11	O70328	O70328 mesocricetu
15	429.5	26.0	111	11	P97731	P97731 rattus sp.
16	172	10.4	372	11	O88507	O88507 mus musculu
17	152.5	9.2	431	11	Q99MF4	Q99mf4 rattus norv
18	149.5	9.0	422	4	Q16542	Q16542 homo sapien
19	148.5	9.0	432	11	P70225	P70225 mus musculu
20	146.5	8.9	432	11	Q64385	Q64385 mus musculu
21	132	8.0	812	10	Q9C6J9	Q9c6j9 arabidopsis
22	129	7.8	229	4	Q14213	Q14213 homo sapien
23	127.5	7.7	622	6	Q9N0J7	Q9n0j7 callithrix
24	122.5	7.4	1277	13	Q98902	Q98902 fugu rubrip
25	118	7.1	229	4	O75269	O75269 homo sapien
26	115	7.0	628	11	Q9JKG1	Q9jkg1 cavia porce
27	113.5	6.9	1148	13	Q9IBA7	Q9iba7 gallus gall
28	113	6.8	428	5	Q8WPM7	Q8wpm7 oikopleura
29	112	6.8	628	11	Q9JKT1	Q9jkt1 cavia porce
30	111.5	6.7	978	6	Q9XS93	Q9xs93 canis famil
31	111	6.7	628	11	Q9JI97	Q9ji97 cavia porce
32	111	6.7	1146	13	Q9I8V6	Q9i8v6 gallus gall
33	109.5	6.6	538	13	Q9DFU0	Q9dfu0 sparus aura
34	109	6.6	838	13	Q90YM1	Q90ym1 brachydanio
35	108.5	6.6	455	4	Q9UIR0	Q9uir0 homo sapien
36	108.5	6.6	626	5	Q22040	Q22040 caenorhabdi
37	108.5	6.6	923	6	O97745	O97745 sus scrofa
38	108.5	6.6	964	6	O97744	O97744 sus scrofa
39	108.5	6.6	964	6	Q9TQQ1	Q9tqq1 sus scrofa
40	108.5	6.6	1197	13	Q90478	Q90478 brachydanio
41	108	6.5	386	6	Q95LF0	Q95lf0 canis famil
42	108	6.5	638	6	Q9TU69	Q9tu69 canis famil
43	107.5	6.5	608	6	Q9N0Y7	Q9n0y7 monodelphis
44	106	6.4	206	4	Q16354	Q16354 homo sapien
45	106	6.4	268	4	Q8TD78	Q8td78 homo sapien

ALIGNMENTS

RESULT 1
Q924V5
ID Q924V5 PRELIMINARY; PRT; 332 AA.
AC Q924V5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Interleukin-12 p40 subunit (IL-12 p40).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY;
RA Shiratori I., Matsumoto M., Tsuji S., Nomura M., Toyoshima K.,
RA Seya T.;
RT "Molecular cloning and functional characterization of guinea pig
RT Interleukin -12.";
RL Int. Immunol. 0:0-0(2001).
DR EMBL; AB025724; BAB63963.1; -.
DR InterPro; IPR003961; FN_1II.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ SEQUENCE 332 AA; 37632 MW; B75D16B23DE8B9B4 CRC64;

Query Match 77.0%; Score 1272.5; DB 11; Length 332;
Best Local Similarity 77.7%; Pred. No. 1.4e-106;
Matches 240; Conservative 22; Mismatches 40; Indels 7; Gaps 3;

```
Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||:||||||||||| ||||| |||||:| ||| ||||| : |::|||||||||||||
Db         23 MWELKKDVYVVELDWHTDAPGETVVLTCNTAEEDGITWTSDRKSDILGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
```

```
Db         83 EDAGGYTCHKGGEVLSRSQLLLHKKEDEIWSTDILKEQKGSNGKTFLKCEARSYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Db        143 WWLTAFGTDVKFSVKGSRGSSDPSGVTCG----EAERVSGDNQEY-KYSVECQEDSACPT 197

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Db        198 AEESLPIEVVVDAIHKFKYENYTSSFYIRDIIKPDPPKNLQLKPSVNSQQVEVSWEYPDT 257

Qy        241 WSTPHSYFSLTFCIQAQG--KNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSW 298

Db        258 WSTPHSYFSLTFLVQTHGKNKNRREKKYELFTDKTSATVSCHKISKVEVRARDRYYSSSW 317

Qy        299 SDWASVSCS 307

Db        318 SEWASVSCS 326


RESULT 2
Q9ET05
ID   Q9ET05      PRELIMINARY;      PRT;   327 AA.
AC   Q9ET05;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p40 subunit.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21424491; PubMed=11533170;
RA   Garcia-Navarro R., Blanco-Urgoiti B., Berraondo P.,
RA   Sanchez De La Rosa R., Vales A., Hervas-Stubbs S., Lasarte J.J.,
RA   Borras F., Ruiz J., Prieto J.;
RT   "Protection against Woodchuck Hepatitis Virus (WHV) Infection by Gene
RT   Gun Coimmunization with WHV Core and Interleukin-12.";
RL   J. Virol. 75:9068-9076(2001).
DR   EMBL; AF288519; AAG01023.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   327 AA;  37140 MW;  42782B3559C224DD CRC64;

  Query Match           76.7%;  Score 1268;  DB 11;  Length 327;
  Best Local Similarity   75.5%;  Pred. No. 3.5e-106;
  Matches  231;  Conservative   34;  Mismatches   39;  Indels    2;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Db         23 IWELEKNVYVVELDWHPDTPGETVVLTCDTPEEDGITWTSEQSSEVLGSGKTLTILVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Db         83 EDAGHYTCHRGGEVLSQMLLLLHKNEDGIWSTDILK-KKEPENKNLVTCEAKNYSGRFTC 141

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Db        142 WWLTAISTDVKFSVKSHRGSSDPQGVTCGEATLSAERVKIEQREYKKYSVQCQEDNACPT 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Db        202 AEETLPITVVVDAVHKLKYENYISSFFIRDIIKPDPPKNLKMKPSKTPQQVEVTWEYPDS 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300

Db        262 WSTPHSYFSLTFSVQVQGK-KKKRSNTLHVDKTSVTVTCQKGAKVSVQARDRYYNSSWSE 320

Qy        301 WASVSC 306

Db        321 WATMSC 326


RESULT 3
Q91ZK7
ID   Q91ZK7      PRELIMINARY;      PRT;   327 AA.
AC   Q91ZK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12 p40 subunit.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pletneva L.M., Bacot S., Blanco J.C., Langley R.J., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF421395; AAL16936.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ   SEQUENCE   327 AA;  37119 MW;  F096702CC950FD56 CRC64;

  Query Match           73.1%;  Score 1208;  DB 11;  Length 327;
  Best Local Similarity   72.7%;  Pred. No. 9.1e-101;
  Matches  224;  Conservative   34;  Mismatches   46;  Indels    4;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Db         23 IWELEKDVYVVEVDWSPGAPGERVVLTCDTSEEDDIIWTSDQSSEVVGSGKTLIVQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Db         83 SDAGQYTCHKGGETLSHSRLLLHKKEDGIWSTDILKDQKDPKNKTFLKCEAANYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Db        143 WWLTAVSTDLKFSLKSSSSSSDSRSVTCGAASLSTEKVTVDQRDYNKYSVACQEDITCPT 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Db        203 AEETLPIELVMEAQHKYKYENYSTGFFIRDIIKPDPPKNLQLKPLKSSQ-VEVSWEYPDS 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKK-DRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 299

Db        262 WSTPHSYFSLKFFVQVYRK--KEKKGESLLVDKPSAKIRCSKGGEVRVRAQDHYYNSSWS 319

Qy        300 DWASVSCS 307

Db        320 EWASVSCN 327


RESULT 4
Q9QUM1
ID   Q9QUM1      PRELIMINARY;      PRT;   335 AA.
AC   Q9QUM1;
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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12B P40 subunit.
GN   IL12B OR LL12B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SJL/J, AND B10.S/J; TISSUE=SPLEEN;
RA   Ma R.Z., Teuscher C.;
RT   "Screening for candidate genes of mouse autoimmnue diseases.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF128215; AAF22556.1; -.
DR   EMBL; AF128214; AAF22555.1; -.
DR   MGD; MGI:96540; Il12b.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   335 AA;  38171 MW;  7D061E116C00FC4A CRC64;

  Query Match             64.3%;  Score 1063.5;  DB 11;  Length 335;
  Best Local Similarity   65.3%;  Pred. No. 1e-87;
  Matches  205;  Conservative   35;  Mismatches   61;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| ||||||||||| |   |:||||||| |||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||||: || | ||:|||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGTASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:||||: ::|  : |||||::||||||||||||| |||:||||||: |||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |         |  | |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGALLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
              ||:|| | || | |
Db        318 YYNSSCSKWACVPC 331


RESULT 5
Q9R278
ID   Q9R278      PRELIMINARY;      PRT;   335 AA.
AC   Q9R278;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p40.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RX   MEDLINE=98273736; PubMed=9613680;
RA   Khalife J., Pierrot C., Cocude C., Cetre C., Godin C., Capron A.;
RT   "Molecular cloning and sequencing of the rat interleukin-12 p40
RT   gene.";
RL   Eur. Cytokine Netw. 9:69-73(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RA   Khalife J., Pierrot C., Cocude C., Cetre C., Godin C., Capron A.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133197; AAD24190.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   335 AA;  38413 MW;  39BF5B49AF191007 CRC64;

  Query Match             64.2%;  Score 1060.5;  DB 11;  Length 335;
  Best Local Similarity   65.0%;  Pred. No. 1.9e-87;
  Matches  204;  Conservative   38;  Mismatches   59;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| :|||||||||| |   |:||||||| |:||
Db         23 MWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||:||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   :|||||::|||    : : ||||  :||||:| :: |||:||:| |||   ||:
Db        140 SWLVHRNTDLKFNIKSSSSSPESRAVTCGRASLSAEKVTLNQRDYEKYSVACQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:||||:||:|  : |||||::|||||||||||| |||:||||||: |||||||||:
Db        200 AEETLPIELVVEAQQQNKYENYSTSFFIRDIIKPDPPKNLQVKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |         |    |:|||:| | | | |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKTKETEEECNQKGAFLVEKTSAEVQC-KGANICVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
              ||:|| | |  | |
Db        318 YYNSSCSKWTCVPC 331


RESULT 6
Q95N82
ID   Q95N82      PRELIMINARY;      PRT;   195 AA.
AC   Q95N82;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 subunit p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Fonfara S., Groene A., Koenig M., Baumgaertner W.;
RT   "Sequence of canine interleukin-12-p40 mRNA in DH82-cells.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF349536; AAK54070.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER       1      1
FT   NON_TER     195    195
SQ   SEQUENCE   195 AA;  21943 MW;  46D77A1570B2F8B9 CRC64;
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  Query Match             57.1%;  Score 944;  DB 6;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 3e-77;
  Matches  176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 79

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS 195


RESULT 7
Q62712
ID   Q62712      PRELIMINARY;      PRT;   268 AA.
AC   Q62712;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin-12p40 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER; TISSUE=CULTURED SPLENOCYTES;
RA   Goodman R.E., Toews G.B.;
RT   "A partial cDNA of the coding region of rat IL-12p40, cloned by RT/PCR
RT   from Staphlococcal endotoxin stimulated splenocytes.";
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U16674; AAA52229.1; -.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain.
FT   NON_TER     268     268
SQ   SEQUENCE   268 AA;  30644 MW;  9370D4CD28D9C73F CRC64;

  Query Match             56.9%;  Score 940;  DB 11;  Length 268;
  Best Local Similarity   70.4%;  Pred. No. 1e-76;
  Matches  176;  Conservative   31;  Mismatches   39;  Indels    4;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| :|||||||||| |   |:||||||| |:||
Db         23 MWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||:||: || | ||:||||:|||||:||   |  ||| ||| || ||||||||
Db         83 LDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKREAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||   :|||||::|||    : : ||||| :||||:| :: |||:||:| |||   ||:
Db        140 SWLVHRNTDLKFNIKSSSSSPESRAVTCGAASLSAEKVTLNQRDYEKYSVACQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:||||:||:|  : |||||::|||||||||||||| |||:|||||: |||||||||:
Db        200 AEETLPIELVVEAQQQNKYENYSTSFFIRDIIKPDPPKNLQVKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSL 250
              ||||||||||
Db        259 WSTPHSYFSL 268


RESULT 8
Q924K7
ID   Q924K7      PRELIMINARY;      PRT;   344 AA.
AC   Q924K7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-12 p40 subunit.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gaucher D., Chadee K.;
RT   "Molecular cloning of gerbil interleukin-12, and its expression as a
RT   bioactive single-chain protein.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288612; AAK83061.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ   SEQUENCE   344 AA;  39375 MW;  21B513448D73E8CB CRC64;

  Query Match             56.1%;  Score 927.5;  DB 11;  Length 344;
  Best Local Similarity   56.6%;  Pred. No. 1.9e-75;
  Matches  184;  Conservative   51;  Mismatches   67;  Indels   23;  Gaps    8;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||:||   |  | ||||| | || |||||  |:::|  ||||:||:||:|
Db         23 IWELEKNVYVVEMDWRSGA-NESVVLTCDTSEEGDITWTKDQTTKVEQSGKTVTIEVKDF 81

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               :||||||||| : ||   ||:|||::| || :|||: | |:|: |||||| ||||||||
Db         82 NEAGQYTCHKGDQTLSHFRLLLHKKKNGYWSNEILKQDKNSENQTFLKCEAANYSGRFTC 141

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRD--YKKYTVECQEGSAC 178
              ||    ||||||:|:|    | : ||||||:|:||:|: | :|   |:|:| |||   |
Db        142 SWLVE-RTDLKFSIKNSSSSPDSRAVTCGAVSLTAEKVKGDEKDGKLKQYSVTCQEDITC 200

Qy        179 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYP 238
              |:|||::|| :|::|  : |||||::|||||||| |||| ||::||||| : ||||||||
Db        201 PTAEETVPIGLVLEAQEQNKYENYSTSFFIRDIITPDPPKNLKVKPLKNDK-VEVSWEYP 259

Qy        239 DTWSTPHSYFSLTFCIQAQG---------KNNREKKDR-LC-------VDKTSAKVVCHK 281
              |:|||||||:| | :  :           :|:| | |  |       || || || | |
Db        260 DSWSTPHSYFALKFYVWTESNKENKMRNTNSNKENKMRNACIQNGTWLVDTTSTKVRC-K 318

Qy        282 DAKIRVQARDRYYSSSWSDWASVSC 306
              | :: |:|:||||:| :|  | | |
Db        319 DGRVCVEAQDRYYNSLYSKHACVPC 343


RESULT 9
Q28232
ID   Q28232      PRELIMINARY;      PRT;   174 AA.
AC   Q28232;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 (Fragment).
GN   IL-12.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lockhart E.A.;
RT   "Cloning and sequencing of cervine IL-12.";
RL   Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; U10160; AAA19658.1; -.
DR   InterPro; IPR002996; CR1A.
FT   NON_TER       1      1
FT   NON_TER     174    174
SQ   SEQUENCE   174 AA;  19684 MW;  389260B3A9067F2E CRC64;

  Query Match             49.5%;  Score 818;  DB 6;  Length 174;
  Best Local Similarity   86.8%;  Pred. No. 5.9e-66;
  Matches  151;  Conservative   14;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         63 AGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW 122
              ||||||||||:|||||||:|||||||||||||:||| | | |||||||:||| |||||
Db          1 AGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWW 60

Qy        123 LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAE 182
              |||||||||||||||| |||:||||||::|| |:| ||:|:|||||||||||||||:||
Db         61 LTAISTDLKFSVKSSRGSSDPRGVTCGAMSLSTEKVIVDHREYKKYTVECQEGSACPAAE 120

Qy        183 ESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWE 236
              |||||||||:|:|||||||||||||||||||||| |||||:|||||| ||||||
Db        121 ESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWE 174


RESULT 10
Q9BG70
ID   Q9BG70      PRELIMINARY;      PRT;   150 AA.
AC   Q9BG70;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Interleukin 12 subunit p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Markus S., Baumgaertner W.;
RT   "Expression of canine interleukin-12 subunit p40 mRNA in a continuous
RT   macrophage cell line.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF333121; AAK01441.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER       1      1
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16780 MW;  A867903EF16083BA CRC64;

  Query Match             48.3%;  Score 799;  DB 6;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-64;
  Matches  150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         27 TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKE 86
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKE 60

Qy         87 DGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGV 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGV 120

Qy        147 TCGAVTLSAERVRVDNRDYKKYTVECQEGS 176
              |||||||||||||||||||||||||||||
Db        121 TCGAVTLSAERVRVDNRDYKKYTVECQEGS 150


RESULT 11
Q9TV09
ID   Q9TV09      PRELIMINARY;      PRT;   149 AA.
AC   Q9TV09;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Interleukin-12 p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT   "Cloning and sequencing of canine IL-12 p40 mRNA.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF091134; AAD46992.1; -.
FT   NON_TER       1      1
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16453 MW;  20E2686B0AA37E26 CRC64;

  Query Match             46.5%;  Score 768;  DB 6;  Length 149;
  Best Local Similarity   98.6%;  Pred. No. 1.6e-61;
  Matches  146;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         47 LGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIF 106
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LGAGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIF 60

Qy        107 LKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYK 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYN 120

Qy        167 KYTVECQEGSACPSAEESLPIEVVVDAI 194
              |||||||||||||||||||||||||||
Db        121 KYTVECQEGSACPSAEESLPIEVVVDAI 148


RESULT 12
Q9Z1Y8
ID   Q9Z1Y8      PRELIMINARY;      PRT;   169 AA.
AC   Q9Z1Y8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   Interleukin 12p40 (Fragment).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069279; PubMed=9824482;
RA   Wicher V., Scarozza A.M., Ramsingh A.I., Wicher K.;
RT   "Cytokine gene expression in skin of susceptible guinea-pig infected
RT   with Treponema pallidum.";
RL   Immunology 95:242-247(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99144670; PubMed=10025978;
RA   Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
RT   "Spontaneous cytokine gene expression in normal guinea pig blood and
RT   tissues.";
RL   Cytokine 10:851-859(1998).
DR   EMBL; AF097507; AAC83805.1; -.
FT   NON_TER       1      1
FT   NON_TER     169    169
SQ   SEQUENCE   169 AA;  19128 MW;  0A2DE7480C1281F5 CRC64;

  Query Match             44.0%;  Score 727.5;  DB 11;  Length 169;
  Best Local Similarity   79.3%;  Pred. No. 8.2e-58;
  Matches  138;  Conservative   11;  Mismatches   20;  Indels    5;  Gaps    2;

Qy         69 HKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST 128
              ||||:||||| ||:||||| |||||||||| |  | ||||||::|||||||||||  |
Db          1 HKGGEVLSRSQLLLHKKEDEIWSTDILKEQKGSNGKTFLKCEARSYSGRFTCWWLTAFGT 60

Qy        129 DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIE 188
              |:||||| ||| ||| |||||     ||||  ||::| ||:|||||| ||||:||||||||
Db         61 DVKFSVKGSRGSSDPSGVTCG----EAERVSGDNQEY-KYSVECQEDSACPTAEESLPIE 115
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Qy        189 VVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWS 242
              |||||||| |||||||||:|||||||||| |||||| ||: ||||||||||||
Db        116 VVVDAIHKFKYENYTSSFYIRDIIKPDPPKNLQLKPSVNSQQVEVSWEYPDTWS 169


RESULT 13
O62779
ID   O62779      PRELIMINARY;      PRT;   143 AA.
AC   O62779;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 p40 subunit (Fragment).
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99322318; PubMed=10391845;
RA   Harley R., Helps C.R., Harbour D.A., Gruffydd-Jones T.J., Day M.J.;
RT   "Cytokine mRNA expression in lesions in cats with chronic
RT   gingivostomatitis.";
RL   Clin. Diagn. Lab. Immunol. 6:471-478(1999).
DR   EMBL; AF054607; AAC15980.1; -.
DR   InterPro; IPR002996; CR1A.
FT   NON_TER       1      1
FT   NON_TER     143    143
SQ   SEQUENCE   143 AA;  16122 MW;  E107DF253F5D4D40 CRC64;

  Query Match             42.0%;  Score 695;  DB 6;  Length 143;
  Best Local Similarity   90.9%;  Pred. No. 5.6e-55;
  Matches  130;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         68 CHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIS 127
              |||| :||| | :|| :|||||||||||:||||||||||||||||||||||||||||
Db          1 CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAIS 60

Qy        128 TDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPI 187
              |||||:|||||| |||||||||| |||||:|||||||||||||||||||||:|||||||
Db         61 TDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPI 120

Qy        188 EVVVDAIHKLKYENYTSSFFIRD 210
              |||||||||||||||||||||||
Db        121 EVVVDAIHKLKYENYTSSFFIRD 143


RESULT 14
O70328
ID   O70328      PRELIMINARY;      PRT;   132 AA.
AC   O70328;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Interleukin-12p40 (Fragment).
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RX   MEDLINE=98234044; PubMed=9573100;
RA   Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT   "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT   analysis of cytokine mRNA expression in experimental visceral
RT   leishmaniasis.";
RL   Infect. Immun. 66:2135-2142(1998).
DR   EMBL; AF046211; AAC40096.1; -.
FT   NON_TER       1      1
FT   NON_TER     132    132
SQ   SEQUENCE   132 AA;  14882 MW;  57355AEA95E57D7E CRC64;

  Query Match             30.7%;  Score 507;  DB 11;  Length 132;
  Best Local Similarity   70.5%;  Pred. No. 4.6e-38;
  Matches   93;  Conservative   18;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         73 KVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKF 132
              | || | ||:||||:|||||||||:||: ||| |||||| ||||||||||||||||||||
Db          1 KTLSHSRLLLHKKENGIWSTDILKDQKDPKNKTFLKCEAANYSGRFTCWWLTAISTDLKF 60

Qy        133 SVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVD 192
              :||||   || : ||||| :||||:| || :||:||:| |||   ||:|||:||| :|::
Db         61 NVKSSSSSSDSRAVTCGAASLSAEKVTVDRKDYQKYSVACQEDITCPTAEETLPIGLVME 120

Qy        193 AIHKLKYENYTS 204
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Db        121 AQHKYKYENYST 132


RESULT 15
P97731
ID   P97731      PRELIMINARY;      PRT;   111 AA.
AC   P97731;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin-12 (Fragment).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96285631; PubMed=8693286;
RA   Mathieson P.W., Gillespie K.M.;
RT   "Cloning of a partial cDNA for rat interleukin-12 (IL-12) and analysis
RT   of IL-12 expression in vivo.";
RL   Scand. J. Immunol. 44:11-14(1996).
DR   EMBL; S82489; AAB37425.2; -.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12689 MW;  BFE9372413B20CB8 CRC64;

  Query Match             26.0%;  Score 429.5;  DB 11;  Length 111;
  Best Local Similarity   73.0%;  Pred. No. 3.6e-31;
  Matches   81;  Conservative   10;  Mismatches   17;  Indels    3;  Gaps    1;

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Db          3 MWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDIHWTSDQRRGVIGSGKTLTITVREF 62

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEA 111
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Job time : 29.2044 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:59:19 ; Search time 10.5307 Seconds
(without alignments)
857.760 Million cell updates/sec

Title: US-09-917-265-53
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Sequence: 1 IWELEKDVYVVELDWHPDAP.....QARDRYYSSSWSDWASVSCS 307

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1418.5	85.8	306	1	US-08-424-682A-1	Sequence 1, Appli
2	1418.5	85.8	328	1	US-08-265-087-2	Sequence 2, Appli
3	1418.5	85.8	328	1	US-08-186-529-2	Sequence 2, Appli
4	1418.5	85.8	328	1	US-08-621-493-2	Sequence 2, Appli
5	1418.5	85.8	328	1	US-08-640-386A-2	Sequence 2, Appli
6	1418.5	85.8	328	2	US-08-965-688-2	Sequence 2, Appli
7	1418.5	85.8	328	2	US-08-751-767A-4	Sequence 4, Appli
8	1418.5	85.8	328	4	US-09-260-173-2	Sequence 2, Appli
9	1418.5	85.8	519	2	US-08-751-767A-12	Sequence 12, Appl
10	1418.5	85.8	540	2	US-08-751-767A-8	Sequence 8, Appli
11	1418.5	85.8	540	2	US-08-751-767A-10	Sequence 10, Appl
12	1058.5	64.0	335	2	US-08-385-335A-15	Sequence 15, Appl
13	1049.5	63.5	335	2	US-08-659-206A-3	Sequence 3, Appli
14	1049.5	63.5	335	2	US-08-659-206A-6	Sequence 6, Appli
15	193	11.7	323	6	5171840-6	Patent No. 5171840
16	193	11.7	323	6	5480796-6	Patent No. 5480796
17	193	11.7	344	6	5171840-7	Patent No. 5171840
18	193	11.7	344	6	5480796-7	Patent No. 5480796
19	193	11.7	468	4	US-08-795-473B-5	Sequence 5, Appli
20	193	11.7	468	4	US-09-439-856-5	Sequence 5, Appli
21	193	11.7	468	6	5171840-2	Patent No. 5171840
22	193	11.7	468	6	5480796-2	Patent No. 5480796
23	170	10.3	372	1	US-07-865-878A-4	Sequence 4, Appli
24	170	10.3	372	1	US-07-676-647-2	Sequence 2, Appli
25	170	10.3	372	1	US-08-449-329-2	Sequence 2, Appli
26	170	10.3	372	2	US-08-445-073-2	Sequence 2, Appli
27	170	10.3	372	2	US-08-585-258-2	Sequence 2, Appli
28	170	10.3	372	2	US-08-603-010-4	Sequence 4, Appli
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31	149.5	9.0	422	4	US-09-151-102-2	Sequence 2, Appli
32	149.5	9.0	422	4	US-08-929-846-2	Sequence 2, Appli
33	146.5	8.9	432	4	US-08-702-665A-3	Sequence 3, Appli
34	146.5	8.9	441	4	US-09-151-102-4	Sequence 4, Appli
35	146.5	8.9	441	4	US-08-929-846-4	Sequence 4, Appli
36	145	8.8	423	4	US-08-702-665A-5	Sequence 5, Appli
37	129	7.8	229	1	US-08-383-750-6	Sequence 6, Appli
38	124.5	7.5	230	5	PCT-US93-09636-6	Sequence 6, Appli
39	121.5	7.4	386	6	5171840-5	Patent No. 5171840
40	121.5	7.4	386	6	5480796-5	Patent No. 5480796
41	120.5	7.3	210	4	US-09-043-785-1	Sequence 1, Appli
42	118	7.1	229	2	US-08-684-687-2	Sequence 2, Appli
43	118	7.1	229	3	US-08-352-678-6	Sequence 6, Appli
44	109.5	6.6	201	6	5171840-11	Patent No. 5171840
45	107.5	6.5	592	4	US-09-000-145-6	Sequence 6, Appli

ALIGNMENTS

```
RESULT 1
US-08-424-682A-1
; Sequence 1, Application US/08424682A
; Patent No. 5650492
;  GENERAL INFORMATION:
;    APPLICANT:  Gately, Maurice K
;    APPLICANT:  Hakimi, John
;    APPLICANT:  Ling, Ping
;    TITLE OF INVENTION:  P40 HOMODIMER OF INTERLEUKIN-12
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,682A
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/087,832
;      FILING DATE:  02-JUL-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  306 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-424-682A-1

  Query Match             85.8%;  Score 1418.5;  DB 1;  Length 306;
  Best Local Similarity   85.0%;  Pred. No. 1.6e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

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              ||||||||||||:||| ||||:||||||||||||||:||| ||| ||:|||||||||||
Db         61 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| ||||||||| |||||||| ||::| :|:||||| ||||:
Db        121 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 179

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
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Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
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RESULT 2
US-08-265-087-2
; Sequence 2, Application US/08265087
; Patent No. 5571515
; GENERAL INFORMATION:
; APPLICANT: Scott, Phillip
; APPLICANT: Trinchieri, Giorgio
; TITLE OF INVENTION: Compositions and Methods for Use of
; TITLE OF INVENTION: IL-12 as an Adjuvant
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,087
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,282
; FILING DATE: 18-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST51AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-265-087-2

Query Match 85.8%; Score 1418.5; DB 1; Length 328;
Best Local Similarity 85.0%; Pred. No. 1.8e-132;
Matches 261; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

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Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:||||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| ||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
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Qy        301 WASVSCS 307
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Db        322 WASVPCS 328
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RESULT 3
US-08-186-529-2
; Sequence 2, Application US/08186529
; Patent No. 5573764
; GENERAL INFORMATION:
; APPLICANT: Sykes, Megan
; APPLICANT: Wolf, Stanley F.
; TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
; TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc., Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,529
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: GI 5225
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8401
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-186-529-2

Query Match 85.8%; Score 1418.5; DB 1; Length 328;
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Matches 261; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

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Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 4
US-08-621-493-2
; Sequence 2, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-621-493-2

  Query Match             85.8%;  Score 1418.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.8e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| |||:|||||||||||||:||| ||| ||:|||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||:::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 5
US-08-640-386A-2
; Sequence 2, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-640-386A-2

  Query Match             85.8%;  Score 1418.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.8e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| |||:|||||||||||||:||| ||| ||:|||||||||||||
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Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:|||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 6
US-08-965-688-2
; Sequence 2, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-965-688-2

  Query Match             85.8%;  Score 1418.5;  DB 2;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.8e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:|||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:|||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 7
US-08-751-767A-4
; Sequence 4, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-4

  Query Match             85.8%;  Score 1418.5;  DB 2;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.8e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
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                ||||||||||||:||| ||||:||||||||||||||:||| ||| ||:||||||||||||
Db          83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy         121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
                |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db         143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy         181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
                |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db         202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy         241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
                |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
Db         262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy         301 WASVSCS 307
                |||| ||
Db         322 WASVPCS 328


RESULT 8
US-09-260-173-2
; Sequence 2, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
;             STREET: Spring House Corporate Center, PO Box 457
;             CITY: Spring House
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/260,173
;             FILING DATE: 01-Mar-1999
;             CLASSIFICATION: <Unknown>
;                             17-JUN-1994
;                             18-APR-1994
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/965,688
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/265,087
;             FILING DATE: 17-JUN-1994
;             APPLICATION NUMBER: US 08/229,282
;             FILING DATE: 18-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: WST51AUSA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-540-9206
;             TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 328 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-260-173-2

  Query Match             85.8%;  Score 1418.5;  DB 4;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.8e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy           1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
                ||||:||||||||||:||||||||||| ||||| |||| ||||||||||||||||||||
Db          23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy          61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
                |||||||||||:||| ||||:||||||||||||||:||| ||| ||:||||||||||||
Db          83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy         121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
                |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db         143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy         181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
                |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db         202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy         241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
                |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
Db         262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy         301 WASVSCS 307
                |||| ||
Db         322 WASVPCS 328


RESULT 9
US-08-751-767A-12
; Sequence 12, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  519 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-12

  Query Match             85.8%;  Score 1418.5;  DB 2;  Length 519;
  Best Local Similarity   85.0%;  Pred. No. 3.4e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy           1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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                ||||:||||||||||:||||||||||| ||||| |||| |||||||||||||||||||
Db          2 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 61

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||:||| ||||:|||||||||||||:||| ||| ||:|||||||||||
Db         62 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 121

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        122 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
               |||||||||:|||:|||||||||||||||||||||||| |||||||||| ||||||||||
Db        181 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
               |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        241 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 300

Qy        301 WASVSCS 307
               |||| ||
Db        301 WASVPCS 307


RESULT 10
US-08-751-767A-8
; Sequence 8, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-8

  Query Match             85.8%;  Score 1418.5;  DB 2;  Length 540;
  Best Local Similarity   85.0%;  Pred. No. 3.6e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||:||| ||||:|||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               |||| ||||| |||||||| |||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
               |||||||||:|||:|||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
               |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
               |||| ||
Db        322 WASVPCS 328


RESULT 11
US-08-751-767A-10
; Sequence 10, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-10

  Query Match             85.8%;  Score 1418.5;  DB 2;  Length 540;
  Best Local Similarity   85.0%;  Pred. No. 3.6e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||:||| ||||:|||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142
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Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||:::| :|:|||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| ||||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328
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RESULT 12
US-08-385-335A-15
; Sequence 15, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WH195-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-385-335A-15

  Query Match             64.0%;  Score 1058.5;  DB 2;  Length 335;
  Best Local Similarity   65.0%;  Pred. No. 8.5e-97;
  Matches  204;  Conservative   35;  Mismatches   62;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| |||||||||| |   |:|||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||: || | ||:|||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:|||||: ::|  : |||||::|||||||||||||| |||:|||||| ||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |         |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
              ||:|| | || | |
Db        318 YYNSSCSKWACVPC 331
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RESULT 13
US-08-659-206A-3
; Sequence 3, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-3

  Query Match             63.5%;  Score 1049.5;  DB 2;  Length 335;
  Best Local Similarity   64.6%;  Pred. No. 6.6e-96;
  Matches  203;  Conservative   35;  Mismatches   63;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| |||||||||| |   |:|||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||: || | ||:|||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:|||||: ::|  : |||||::|||||||||||||| |||:|||||| ||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258
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Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |   : |        |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
               |:|| | || | |
Db        318 CYNSSCSKWACVPC 331


RESULT 14
US-08-659-206A-6
; Sequence 6, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-6

  Query Match             63.5%;  Score 1049.5;  DB 2;  Length 335;
  Best Local Similarity   64.6%;  Pred. No. 6.6e-96;
  Matches  203;  Conservative   35;  Mismatches   63;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :||||||||||:|| |||||| | ||| ||||||||||| |   |:|||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:|||| ::|  : |||||::||||||||||||| |||:|||||: |||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |   : |        |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
               |:|| | || | |
Db        318 CYNSSCSKWACVPC 331


RESULT 15
5171840-6
;Patent No. 5171840
;    APPLICANT: KISHIMOTO, TADAMITSU
;    TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
;STIMULATORY FACTOR-2
;    NUMBER OF SEQUENCES: 11
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/298,694
;      FILING DATE: 19-JAN-1989
;SEQ ID NO:6:
;      LENGTH: 323
5171840-6

  Query Match             11.7%;  Score 193;  DB 6;  Length 323;
  Best Local Similarity   22.2%;  Pred. No. 4.6e-11;
  Matches   69;  Conservative   59;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         20 PGEMVVLTCHTPEEDD---ITW------TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK 70
              ||: | |||   | :|   : |        :  |   | |: | ::  :  |:| |:|::
Db         39 PGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR 98

Qy         71 GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW-------L 123
               |:     ||:          |: |: :     | |  |:     | |       |
Db         99 AGRPAGTVHLLV----------DVPPEEPQ------LSCFRKSPLSNVVCEWGPRSTPSL 142

Qy        124 T--AISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS---AC 178
              |  |:    ||    :  | :|    |-                 :|: | |: |   |
Db        143 TTKAVLLVRKFQNSPAEDFQEP----C-----------------QYSQESQKFSCQLAV 180

Qy        179 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEY 237
              |  : |  |  :  |       : | :|    |::|||| |: :  : :| | : |:|:
Db        181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240

Qy        238 PDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDA------KIRVQARD 291
              | :|::  |:: | | :: : : ::     :  |     |:   ||       ::::|::
Db        241 PHSWNS--SFYRLRFELRYRAERSKTFTTWMVKDLQHHCVI--HDAWSGLRHVVQLRAQE 296

Qy        292 RYYSSSWSDWA 302
               :    ||:|:
Db        297 EFGQGEWSEWS 307


Search completed: July 15, 2003, 11:10:00
Job time : 11.5307 secs
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